

SEQUENCE LISTING

<110> Aharoni, Asaph
 Lucker, Joost
 Verhoeven, Harrie A.
 van Tunen, Arjen J.
 O'Connell, Ann P.

<120> Fruit Flavour Related Genes And Use Thereof

<130> 160721

<140> pct/nl99/00737
 <141> 1999-12-02

<150> EP 98204018.0
 <151> 1998-12-02

<150> EP 99200739.3
 <151> 1999-03-12

<160> 47

<170> PatentIn Ver. 2.1

<210> 1
 <211> 1632
 <212> DNA
 <213> Fragaria x ananassa

<220>

<221> CDS
 <222> (16)..(1371)
 <223> cDNA

<220>

<223> Strawberry alcohol acyl transferase

<400> 1
 acctactttg ccaaa atg gag aaa att gag gtc agt ata aat tcc aaa cac 51
 Met Glu Lys Ile Glu Val Ser Ile Asn Ser Lys His
 1 5 10

acc atc aaa cca tca act tcc tct aca cca ctt cag cct tac aag ctt 99
 Thr Ile Lys Pro Ser Thr Ser Ser Thr Pro Leu Gln Pro Tyr Lys Leu
 15 20 25

acc ctc ctg gac cag ctc act cct ccg gcg tat gtc ccc atc gtg ttc 147
 Thr Leu Leu Asp Gln Leu Thr Pro Pro Ala Tyr Val Pro Ile Val Phe
 30 35 40

ttc tac ccc att act gac cat gac ttc aat ctt cct caa acc cta gct 195
 Phe Tyr Pro Ile Thr Asp His Asp Phe Asn Leu Pro Gln Thr Leu Ala
 45 50 55 60

gac tta aga caa gcc ctt tcg gag act ctc act ttg tac tat cca ctc 243
 Asp Leu Arg Gln Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu
 65 70 75

tct gga agg gtc aaa aac aac cta tac atc gat gat ttt gaa gaa ggt 291
 Ser Gly Arg Val Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly
 80 85 90

gtc cca tac ctt gag gct cga gtg aat tgt gac atg act gat ttt cta	339
Val Pro Tyr Leu Glu Ala Arg Val Asn Cys Asp Met Thr Asp Phe Leu	
95 100 105	
agg ctt cgaaatc gag tgc ctt aat gag ttt gtt cca ata aaa cca	387
Arg Leu Arg Lys Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro	
110 115 120	
ttt agt atg gaa gca ata tct gat gag cgt tac ccc ttg ctt gga gtt	435
Phe Ser Met Glu Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val	
125 130 135 140	
caa gtc aac gtt ttc gat tct gga ata gca atc ggt gtc tcc gtc tct	483
Gln Val Asn Val Phe Asp Ser Gly Ile Ala Ile Gly Val Ser Val Ser	
145 150 155	
cac aag ctc atc gat gga gga acg gca gac tgt ttt ctc aag tcc tgg	531
His Lys Leu Ile Asp Gly Gly Thr Ala Asp Cys Phe Leu Lys Ser Trp	
160 165 170	
ggt gct gtt ttt cga ggg tgt cgt gaa aat atc ata cat cct agt ctc	579
Gly Ala Val Phe Arg Gly Cys Arg Glu Asn Ile Ile His Pro Ser Leu	
175 180 185	
tct gaa gca gca ttg ctt ttc cca ccg aga gat gac ttg cct gaa aag	627
Ser Glu Ala Ala Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys	
190 195 200	
tat gtc gat cag atg gaa gcg tta tgg ttt gcc gga aaa aaa gtt gct	675
Tyr Val Asp Gln Met Glu Ala Leu Trp Phe Ala Gly Lys Lys Val Ala	
205 210 215 220	
aca agg aga ttt gta ttt ggt gtg aaa gcc ata tct tca att caa gat	723
Thr Arg Arg Phe Val Phe Gly Val Lys Ala Ile Ser Ser Ile Gln Asp	
225 230 235	
gaa gcg aag agc gag tcc gtg ccc aag cca tca cga gtt cat gcc gtc	771
Glu Ala Lys Ser Glu Ser Val Pro Lys Pro Ser Arg Val His Ala Val	
240 245 250	
act ggt ttt ctc tgg aaa cat cta atc gct gct tct cgg gca cta aca	819
Thr Gly Phe Leu Trp Lys His Leu Ile Ala Ala Ser Arg Ala Leu Thr	
255 260 265	
tca ggt act act tca aca aga ctt tct ata gcg gcc cag gca gtg aac	867
Ser Gly Thr Thr Ser Thr Arg Leu Ser Ile Ala Ala Gln Ala Val Asn	
270 275 280	
tta aga aca cgg atg aac atg gag aca gtg ttg gat aat gcc act gga	915
Leu Arg Thr Arg Met Asn Met Glu Thr Val Leu Asp Asn Ala Thr Gly	
285 290 295 300	
aac ttg ttc tgg tgg gca cag gcc ata cta gag cta agt cat aca aca	963
Asn Leu Phe Trp Trp Ala Gln Ala Ile Leu Glu Leu Ser His Thr Thr	
305 310 315	
cca gag atc agt gat ctt aag ctg tgt gac ttg gtt aac ttg ctc aat	1011
Pro Glu Ile Ser Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn	
320 325 330	
gga tct gtc aaa caa tgt aac ggt gat tac ttt gag act ttc aag ggt	1059
Gly Ser Val Lys Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Lys Gly	

335

340

345

aaa gag gga tat gga aga atg tgc gag tat cta gat ttt cag agg act	1107
Lys Glu Gly Tyr Gly Arg Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr	
350 355 360	
atg agt tct atg gaa cca gca ccg gat att tat tta ttc tcg agc tgg	1155
Met Ser Ser Met Glu Pro Ala Pro Asp Ile Tyr Leu Phe Ser Ser Trp	
365 370 375 380	
act aat ttt ttc aac cca ctt gat ttt gga tgg ggg agg aca tca tgg	1203
Thr Asn Phe Phe Asn Pro Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp	
385 390 395	
att gga gtt gca gga aaa att gaa tct gca agt tgc aag ttc ata ata	1251
Ile Gly Val Ala Gly Lys Ile Glu Ser Ala Ser Cys Lys Phe Ile Ile	
400 405 410	
tta gtt cca aca caa tgc ggt tct gga att gaa gcg tgg gtg aat cta	1299
Leu Val Pro Thr Gln Cys Gly Ser Gly Ile Glu Ala Trp Val Asn Leu	
415 420 425	
gaa gaa gag aaa atg gct atg cta gaa caa gat ccc cat ttt cta gcg	1347
Glu Glu Glu Lys Met Ala Met Leu Glu Gln Asp Pro His Phe Leu Ala	
430 435 440	
tta gca tct cca aag acc tta att taaaagatatt gattaagaaa gattatgtgg	1401
Leu Ala Ser Pro Lys Thr Leu Ile	
445 450	
ctcgtgcaat gtttcgattt tgcaagtgaat aaggtttaaa ttatgttacc agccaatcaa	1461
taaaatgcaa gtatgataga ctttgcctac gtatgttacc cgaatgtgtt tccatatgct	1521
tgttaaccaat atagctcttt attgtaacaa atgctctatt aagcttcttag ctataaagtt	1581
atttatctat taaaaataaaa actatggaag ttttacccaaa aaaaaaaaaa a	1632
<210> 2	
<211> 1613	
<212> DNA	
<213> Citrus limon	
<220>	
<221> CDS	
<222> (125)..(1426)	
<223> cDNA	
<220>	
<223> Citrus limon alcohol acyl transferase	
<400> 2	
cttattttaaa agttcatcaa caaattgttc taccacttac catttctcat agctctgcaa	60
gttcggattt gactcttct ctttcctca ttccggccgg tggatgttacatttgg	120
caca atg aaa att cac gtt aag gag tca aca att ata cgc cct gct caa	169
Met Lys Ile His Val Lys Glu Ser Thr Ile Ile Arg Pro Ala Gln	
1 5 10 15	
gaa aca ccc aag cat cgc cta caa ata tcc gac cta gac atg att gtg	217
Glu Thr Pro Lys His Arg Leu Gln Ile Ser Asp Leu Asp Met Ile Val	

20	25	30	
cca tcc aat tac gtt ccc agt gtg tat ttc tat cgg cgg tcc agt gac Pro Ser Asn Tyr Val Pro Ser Val Tyr Phe Tyr Arg Arg Ser Ser Asp 35	40	45	265
tgc acc gat ttt ttt gaa gtt ggt ttg ctg aag aag gct ctg agc gaa Cys Thr Asp Phe Phe Glu Val Gly Leu Leu Lys Lys Ala Leu Ser Glu 50	55	60	313
gtt ctt gtg ccg ttt tac ccc gtt gcc gga agg ttg cag aag gat gaa Val Leu Val Pro Phe Tyr Pro Val Ala Gly Arg Leu Gln Lys Asp Glu 65	70	75	361
aat cgc aaa att gag att cta tgt aac gga gag gga gtt ttg ttt ctg Asn Arg Lys Ile Glu Ile Leu Cys Asn Gly Glu Gly Val Leu Phe Leu 80	85	90	409
gag gcc gaa aca agt tgt ggt att gat gat ttc ggt gac ttc tca caa Glu Ala Glu Thr Ser Cys Gly Ile Asp Asp Phe Gly Asp Phe Ser Gln 100	105	110	457
ggc tcg aaa ctc ctg acg ctt gtt cca act gtt ggt gat aca aag gat Gly Ser Lys Leu Leu Thr Leu Val Pro Thr Val Gly Asp Thr Lys Asp 115	120	125	505
ata tcc tcc cat cca ctc ttg atg gca cag gta act tat ttc aaa tgt Ile Ser Ser His Pro Leu Leu Met Ala Gln Val Thr Tyr Phe Lys Cys 130	135	140	553
gga ggc gtt tgt gtt gga act aga gtg aat cat aca ctg gta gat gga Gly Gly Val Cys Val Gly Thr Arg Val Asn His Thr Leu Val Asp Gly 145	150	155	601
gct tca gcg tac cat atc atc aac tca tgg gcg gag acg acg cgt ggc Ala Ser Ala Tyr His Ile Ile Asn Ser Trp Ala Glu Thr Thr Arg Gly 160	165	170	649
gtt cct att agc act caa cca ttc tat gat cgg acc ata ctg agt gtt Val Pro Ile Ser Thr Gln Pro Phe Tyr Asp Arg Thr Ile Leu Ser Val 180	185	190	697
ggg gtt cca act tct ccc aaa ttc cat cac att gaa tat gac ccg cct Gly Val Pro Thr Ser Pro Lys Phe His His Ile Glu Tyr Asp Pro Pro 195	200	205	745
cct tcc atg aac gct cct cct acc caa aat cct gaa atc att tct acc Pro Ser Met Asn Ala Pro Pro Thr Gln Asn Pro Glu Ile Ile Ser Thr 210	215	220	793
gca atc ctt aac cta tca ctt gat caa atc cac acc ctc aaa gag aaa Ala Ile Leu Asn Leu Ser Leu Asp Gln Ile His Thr Leu Lys Glu Lys 225	230	235	841
tct aag aca gat cat gaa ccc aac gtc aag tat agt agg atg gcg atc Ser Lys Thr Asp His Glu Pro Asn Val Lys Tyr Ser Arg Met Ala Ile 240	245	250	889
cta gca gca cat atc tgg cgt agc atg tgt aaa gcg cgc gga tta tct Leu Ala Ala His Ile Trp Arg Ser Met Cys Lys Ala Arg Gly Leu Ser 260	265	270	937

gat gat caa gtt agc aag tta cac ttt cct aca gac gga cga cag aga	985		
Asp Asp Gln Val Ser Lys Leu His Phe Pro Thr Asp Gly Arg Gln Arg			
275	280	285	
ttg aat cca cca ctc ccg cct gga tat ttt gga aat gta att ttc acc	1033		
Leu Asn Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr			
290	295	300	
acg tcg ttg acg gct tca tcg ggt gat atc cta agt gaa cca ttg aat	1081		
Thr Ser Leu Thr Ala Ser Ser Gly Asp Ile Leu Ser Glu Pro Leu Asn			
305	310	315	
cat act gtt gaa aga att caa aaa gca tta aag cgg atg gac gat gag	1129		
His Thr Val Glu Arg Ile Gln Lys Ala Leu Lys Arg Met Asp Asp Glu			
320	325	330	335
tat ttg aaa tca gca ctt gct tac cta aag caa cag cct gat tta aat	1177		
Tyr Leu Lys Ser Ala Leu Ala Tyr Leu Lys Gln Gln Pro Asp Leu Asn			
340	345	350	
gct cta cgg aaa gga ggc cac att tac aag tgc cct aac ctc aat atc	1225		
Ala Leu Arg Lys Gly Gly His Ile Tyr Lys Cys Pro Asn Leu Asn Ile			
355	360	365	
gtc aat ttg gca aat atg cca atg tat gtt gcg aat ttt gga tgg ggc	1273		
Val Asn Leu Ala Asn Met Pro Met Tyr Val Ala Asn Phe Gly Trp Gly			
370	375	380	
cag ccg ata ttt gcg agg atc gtt aac aca tat tat gaa ggg ata gca	1321		
Gln Pro Ile Phe Ala Arg Ile Val Asn Thr Tyr Tyr Glu Gly Ile Ala			
385	390	395	
cat.att tat cca agt ccg agc aat gat ggg acc ttg tca gtg gtt ata	1369		
His Ile Tyr Pro Ser Pro Ser Asn Asp Gly Thr Leu Ser Val Val Ile			
400	405	410	415
aac tcg gta gcc gat cac atg cag ctg ttc aag aag ttc ttt tac gag	1417		
Asn Ser Val Ala Asp His Met Gln Leu Phe Lys Lys Phe Phe Tyr Glu			
420	425	430	
atc ttt gat taaggtatga aagacctagg tattttatat tttctagaaa	1466		
Ile Phe Asp			
tgtcactttt tttttttttt ttttttgggg gcgcaaatgt tgtcttactt ggaattttat	1526		
atattttaat ccatgttttt atggaaggca gtggtgttgc aaaaaaaaaa aaaaaaaaaa	1586		
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1613		
<210> 3			
<211> 1775			
<212> DNA			
<213> Fragaria x ananassa			
<220>			
<221> CDS			
<222> (37)..(1410)			
<223> cDNA			
<220>			
<223> Strawberry thiolase			

<400> 3
 cgctcctttg atttccttgc ttcaattatc aagagt atg gag aaa gcg atc aac 54
 Met Glu Lys Ala Ile Asn
 1 5
 agg cag aag gtt ctc ctc gac cat ctc cga cct tct tct tct tcc gac 102
 Arg Gln Lys Val Leu Leu Asp His Leu Arg Pro Ser Ser Ser Ser Asp
 10 15 20
 gac tct tct ctc tcc gcg tcg gta tgt gcg gct ggg gat agc gct gcg 150
 Asp Ser Ser Leu Ser Ala Ser Val Cys Ala Ala Gly Asp Ser Ala Ala
 25 30 35
 tat gct agg aat cat gtc ttt ggg gac gat gtc gtc atc gtt gca gct 198
 Tyr Ala Arg Asn His Val Phe Gly Asp Asp Val Val Ile Val Ala Ala
 40 45 50
 ttt cgc act cca ctc tgc aag gct aag cgt ggc ggc ttc aag tat act 246
 Phe Arg Thr Pro Leu Cys Lys Ala Lys Arg Gly Gly Phe Lys Tyr Thr
 55 60 65 70
 tat gct gat gat ctc ctc gca cct gtc ctc aag gcc gtg gtt gag aaa 294
 Tyr Ala Asp Asp Leu Leu Ala Pro Val Leu Lys Ala Val Val Glu Lys
 75 80 85
 acc aat ctc aat ccc aag gaa gtc ggg gat att gtt gtc ggt acc gtc 342
 Thr Asn Leu Asn Pro Lys Glu Val Gly Asp Ile Val Val Gly Thr Val
 90 95 100
 ttg gcc cca gga tct cag aga gct agc gaa tgc agg atg gct gct ttc 390
 Leu Ala Pro Gly Ser Gln Arg Ala Ser Glu Cys Arg Met Ala Ala Phe
 105 110 115
 tat gct ggc ttc cct gag act gtg ccg gtt aga act gtg aac aga caa 438
 Tyr Ala Gly Phe Pro Glu Thr Val Pro Val Arg Thr Val Asn Arg Gln
 120 125 130
 tgt tcg tct ggc ctc caa gca gtt gct gat gtt gct gct gcc att aga 486
 Cys Ser Ser Gly Leu Gln Ala Val Ala Asp Val Ala Ala Ala Ile Arg
 135 140 145 150
 gca ggg ttt tat gat att ggc att ggt gct ggt ttg gaa tcc atg act 534
 Ala Gly Phe Tyr Asp Ile Gly Ile Gly Ala Gly Leu Glu Ser Met Thr
 155 160 165
 gca aac cca atg gca tgg gaa ggg gat gtt aat cct aaa gta aag atc 582
 Ala Asn Pro Met Ala Trp Glu Gly Asp Val Asn Pro Lys Val Lys Ile
 170 175 180
 ttt gaa caa gcc cag aat tgc ctt ctt cct atg gga gtc acc tca gaa 630
 Phe Glu Gln Ala Gln Asn Cys Leu Leu Pro Met Gly Val Thr Ser Glu
 185 190 195
 aat gtt gct cat cgt ttt ggt gtt tca aga cag gag caa gat cag gct 678
 Asn Val Ala His Arg Phe Gly Val Ser Arg Gln Glu Gln Asp Gln Ala
 200 205 210
 gca gtt gac tct cat aga aag gca gct gct gct gct gct gct ggt aga 726
 Ala Val Asp Ser His Arg Lys Ala Ala Ala Ala Ala Ala Gly Arg
 215 220 225 230
 ttt aaa gat gaa atc atc cct gtg gca acc aag att gtt gat cca aaa 774

Phe Lys Asp Glu Ile Ile Pro Val Ala Thr Lys Ile Val Asp Pro Lys			
235	240	245	
tct ggt gat gag aaa cct gtt aca atc tct gtt gat gat ggg att cga		822	
Ser Gly Asp Glu Lys Pro Val Thr Ile Ser Val Asp Asp Gly Ile Arg			
250	255	260	
aac aca aca ttg gcg gac cta gca aag ctg aag cct gtg ttt aag aaa		870	
Asn Thr Thr Leu Ala Asp Leu Ala Lys Leu Lys Pro Val Phe Lys Lys			
265	270	275	
gat ggg acc acc act gct ggt aat tct agt caa gtt agt gat ggt gct		918	
Asp Gly Thr Thr Ala Gly Asn Ser Ser Gln Val Ser Asp Gly Ala			
280	285	290	
gga gct gtt ctc ttg atg aag aga agt gtt gcc gac caa aaa gga ttg		966	
Gly Ala Val Leu Leu Met Lys Arg Ser Val Ala Asp Gln Lys Gly Leu			
295	300	305	310
ccg att ctt ggt gta ttc agg aat ttt gtt gct gtt ggt gtg gat cct		1014	
Pro Ile Leu Gly Val Phe Arg Asn Phe Val Ala Val Gly Val Asp Pro			
315	320	325	
gcc atc atg ggt gtt ggc cca gct gct gca att cca gtt gca gtt aag		1062	
Ala Ile Met Gly Val Gly Pro Ala Ala Ala Ile Pro Val Ala Val Lys			
330	335	340	
gca gct ggt tta gag ctt gat gat att gac ctt ttt gag ata aat gag		1110	
Ala Ala Gly Leu Glu Leu Asp Asp Ile Asp Leu Phe Glu Ile Asn Glu			
345	350	355	
gct ttt gca tcc caa ttt gtg tat tgc cgt aac aag ctg gga ctt gat		1158	
Ala Phe Ala Ser Gln Phe Val Tyr Cys Arg Asn Lys Leu Gly Leu Asp			
360	365	370	
cca gaa aaa atc aat gtt aac gga ggt gca atg gcc atc ggc cat cca		1206	
Pro Glu Lys Ile Asn Val Asn Gly Gly Ala Met Ala Ile Gly His Pro			
375	380	385	390
ctt ggt gca aca ggt gcc cgg tgt gtt gcc act ctt ttg cat gag atg		1254	
Leu Gly Ala Thr Gly Ala Arg Cys Val Ala Thr Leu Leu His Glu Met			
395	400	405	
aag cgt cgt ggt aaa gac tgc cgc tat gga gtg atc tca atg tgc ata		1302	
Lys Arg Arg Gly Lys Asp Cys Arg Tyr Gly Val Ile Ser Met Cys Ile			
410	415	420	
ggc aca ggg atg ggt gca gcc gct gtt ttt gaa aga gga gac cgg acc		1350	
Gly Thr Gly Met Gly Ala Ala Val Phe Glu Arg Gly Asp Arg Thr			
425	430	435	
gat gaa ctc tgc aat gct cgc aag gtt gaa tca ctc aac ttc tta tcc		1398	
Asp Glu Leu Cys Asn Ala Arg Lys Val Glu Ser Leu Asn Phe Leu Ser			
440	445	450	
aag gat gtt cgg tagtagagaa tggtagtga caggagctat tccaatcaat		1450	
Lys Asp Val Arg			
455			
aatgttttgtt ggagtctgaa aatcatagta aagcactgga ataacgttgc taagttttc	1510		
gttgggtact accttgttta ttggatgga atacacatgt agttggtttgc ttctcccaga	1570		

cctcccaactt gttggcatat tcattttgt ccaacctaaa aagttccatt ttataggact 1630
 tcatctcaat aacattgggt ttgcgccact aaagcagtgc ctaaaactgt aattggtaa 1690
 ttttggata cctgttgct actttcttt tctaagttaa tcaagccctg cccacctcat 1750
 ataaaaaaaaaaaaaaa aaaaa 1775

 <210> 4
 <211> 2141
 <212> DNA
 <213> Fragaria x ananassa

 <220>
 <221> CDS
 <222> (78)..(1892)
 <223> cDNA

 <220>
 <223> Strawberry pyruvate decarboxylase

 <400> 4
 attttcactc agagtctcaa tcattcatca caaaaaattcc catttgatca caaaaaagtt 60

 tcaaccttta aacctcc atg gac acc aag att ggc tcc atc gac gtc tgc 110
 Met Asp Thr Lys Ile Gly Ser Ile Asp Val Cys
 1 5 10

 aaa acc gag aac cac gac gtc ggt tgg tta cca aac agc gcc acc tcc 158
 Lys Thr Glu Asn His Asp Val Gly Cys Leu Pro Asn Ser Ala Thr Ser
 15 20 25

 acc gtt caa aac tca gtc cct tcc acc tcc ctc agc tcc gcc gac gcc 206
 Thr Val Gln Asn Ser Val Pro Ser Thr Ser Leu Ser Ser Ala Asp Ala
 30 35 40

 acc ctc ggc cgc cac ctg gca cgc cgc ctc gtt caa atc ggc gtc acc 254
 Thr Leu Gly Arg His Leu Ala Arg Arg Leu Val Gln Ile Gly Val Thr
 45 50 55

 gac gtc ttc acc gtc ccc ggc gac ttc aac ttg acc ctt ctt gac cac 302
 Asp Val Phe Thr Val Pro Gly Asp Phe Asn Leu Thr Leu Leu Asp His
 60 65 70 75

 ctc atc gcc gag ccc ggc ctc acc aac att ggc tgc tgc aac gag ctc 350
 Leu Ile Ala Glu Pro Gly Leu Thr Asn Ile Gly Cys Cys Asn Glu Leu
 80 85 90

 aac gcc ggg tac gcc gac ggc tac gcg cgg tcg cgt ggc gtc ggc 398
 Asn Ala Gly Tyr Ala Ala Asp Gly Tyr Ala Arg Ser Arg Gly Val Gly
 95 100 105

 gcg tgc gtg act ttc act gtt ggt gga ctg agt gtg ctg aac gcg 446
 Ala Cys Val Val Thr Phe Thr Val Gly Gly Leu Ser Val Leu Asn Ala
 110 115 120

 atc gcc ggc gcg tat agt gag aat ttg ccg gtg att tgt att gtt ggt 494
 Ile Ala Gly Ala Tyr Ser Glu Asn Leu Pro Val Ile Cys Ile Val Gly
 125 130 135

 ggg ccc aac tct aac gat tat ggg act aac ccg att ctt cac cat act 542
 Gly Pro Asn Ser Asn Asp Tyr Gly Thr Asn Arg Ile Leu His His Thr

140	145	150	155
att ggg ttg ccg gac ttc agt caa gag ctc cg ^g tgc ttt cag acc gtg Ile Gly Leu Pro Asp Phe Ser Gln Glu Leu Arg Cys Phe Gln Thr Val			590
160	165	170	
act tgc ttt cag gct gtg gtg aat aat ctg gag gat gca cat gag atg Thr Cys Phe Gln Ala Val Val Asn Asn Leu Glu Asp Ala His Glu Met			638
175	180	185	
att gat act gca att tcg act gcg ttg aaa gaa agc aag cct gtg tat Ile Asp Thr Ala Ile Ser Thr Ala Leu Lys Glu Ser Lys Pro Val Tyr			686
190	195	200	
atc agc att ggc tgc aac ttg gct ggg att cct cat cct act ttc agc Ile Ser Ile Gly Cys Asn Leu Ala Gly Ile Pro His Pro Thr Phe Ser			734
205	210	215	
cgt gaa cct gtt cca ttt tca ttg tct cca aaa ttg agc aat aag tgg Arg Glu Pro Val Pro Phe Ser Leu Ser Pro Lys Leu Ser Asn Lys Trp			782
220	225	230	235
gga tta gag gct gca gtg gag gct gct gca gag ttc ttg aac aag gca Gly Leu Glu Ala Ala Val Glu Ala Ala Ala Glu Phe Leu Asn Lys Ala			830
240	245	250	
gtg aag cca gtt atg gtg ggc ggg ccc aaa ctg cgc tct gca cat gct Val Lys Pro Val Met Val Gly Gly Pro Lys Leu Arg Ser Ala His Ala			878
255	260	265	
gg ^t gat gcc ttt gtt gaa ctg gct gat gct tct gga ttt gct ctg gct Gly Asp Ala Phe Val Glu Leu Ala Asp Ala Ser Gly Phe Ala Leu Ala			926
270	275	280	
gtg atg cca tca gca aag ggg caa gtg cca gag cac cac ccc cat ttc Val Met Pro Ser Ala Lys Gly Gln Val Pro Glu His His Pro His Phe			974
285	290	295	
atc gga acg tac tgg ggt gct gtg agc act gcc ttt tgt gct gag att Ile Gly Thr Tyr Trp Gly Ala Val Ser Thr Ala Phe Cys Ala Glu Ile			1022
300	305	310	315
gtg gag tct gca gat gca tac ttg ttt gct ggg ccg att ttc aat gag Val Glu Ser Ala Asp Ala Tyr Leu Phe Ala Gly Pro Ile Phe Asn Asp			1070
320	325	330	
tac agc tca gtt ggg tac tcg ctc ctt ctc aag aaa gag aag gcg atc Tyr Ser Ser Val Gly Tyr Ser Leu Leu Leu Lys Lys Glu Lys Ala Ile			1118
335	340	345	
att gtg cag cca gat cgt gtg acg ata ggg aat ggc cct aca ttt ggt Ile Val Gln Pro Asp Arg Val Thr Ile Gly Asn Gly Pro Thr Phe Gly			1166
350	355	360	
tgt gtt ctc atg aag gat ttc ctc tta ggc cta gca aag aag ctg aag Cys Val Leu Met Lys Asp Phe Leu Leu Gly Leu Ala Lys Lys Leu Lys			1214
365	370	375	
cat aac aac act gct cat gag aac tac cgc agg atc ttt gtg cct gat His Asn Asn Thr Ala His Glu Asn Tyr Arg Arg Ile Phe Val Pro Asp			1262
380	385	390	395

ggc cac cct ctg aag gct gca ccc aaa gaa cct ttg agg gtt aat gtt Gly His Pro Leu Lys Ala Ala Pro Lys Glu Pro Leu Arg Val Asn Val 400 405 410	1310
ctg ttc aaa cac att cag aat atg ctg tca gct gaa acc gct gtg att Leu Phe Lys His Ile Gln Asn Met Leu Ser Ala Glu Thr Ala Val Ile 415 420 425	1358
gct gag aca ggg gac tca tgg ttt aac tgt cag aag ctg aaa ttg cca Ala Glu Thr Gly Asp Ser Trp Phe Asn Cys Gln Lys Leu Lys Leu Pro 430 435 440	1406
ccc ggc tgc ggg tat gag ttc caa atg caa tat gga tca att ggt tgg Pro Gly Cys Gly Tyr Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp 445 450 455	1454
tca gtt gga gca act ctt ggg tat gct cag gct gta cct gag aag cga Ser Val Gly Ala Thr Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg 460 465 470 475	1502
gtg att tct ttc att ggt gat ggg agc ttc cag gtg act gct caa gat Val Ile Ser Phe Ile Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp 480 485 490	1550
gtg tcc aca atg att cga aat gga cag aga acc att att ttc ctg ata Val Ser Thr Met Ile Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile 495 500 505	1598
aac aat ggt gga tac acc att gaa gtg gaa atc cat gat gga cca tac Asn Asn Gly Gly Tyr Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr 510 515 520	1646
aat gtg atc aag aac tgg aac tac act gga ctg gtt gat gca atc cac Asn Val Ile Lys Asn Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His 525 530 535	1694
aat ggg gaa ggc aag tgc tgg aca acc aag gtg cgt tgc gaa gag gag Asn Gly Glu Gly Lys Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu 540 545 550 555	1742
ctg att gaa gca ata gag act gca aat gga ccc aag aag gat agc ttc Leu Ile Glu Ala Ile Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe 560 565 570	1790
tgc ttc att gag gtg att gtt cac aag gat gat acc agc aaa gag ttg Cys Phe Ile Glu Val Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu 575 580 585	1838
ctt gag tgg ggg tct agg gtt tct gct gcc aac agc cgc cca cct aat Leu Glu Trp Gly Ser Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn 590 595 600	1886
cct cag taaaactctc ctgtgtcata tgaaggcctt cattcacatt cacagattta Pro Gln 605	1942
gatcaagcca agctcttgtg caaattttcc ttatgtttt cctgtcaact ggagaatgg 2002	
gtctgtcaag tttttttac actacagtga tttctggttt gtctgtatat ttcccttctga 2062	
atatttagtat cttctgattt ttcaattgtat caaattctgt gatcctaaat ggtttgtgga 2122	

aaaaaaaaaaa aaaaaaaaa

2141

<210> 5
<211> 1415
<212> DNA
<213> Fragaria x ananassa

<220>
<221> CDS
<222> (56)..(1054)
<223> cDNA

<220>
<223> Strawberry alcohol dehydrogenase

<400> 5
taatctagct tctgcaccaa aactatcaga taattaagaa tctgccacag agaaa atg 58
Met 1
gtg atg tct atc gag cag gaa cac ccc aag aag gca tct gga tgg gct 106
Val Met Ser Ile Glu Gln Glu His Pro Lys Lys Ala Ser Gly Trp Ala
5 10 15
gca aga gat tca tct ggt gtt ctc tct ccc ttc agt ttc tcc aga agg 154
Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Ser Arg Arg Arg
20 25 30
gaa acc gga gag aaa gac gtg acg ttc aaa gtg atg tac tgt ggg att 202
Glu Thr Gly Glu Lys Asp Val Thr Phe Lys Val Met Tyr Cys Gly Ile
35 40 45
tgc cat tcg gac ctt cac atg gtc aag aat gaa tgg ggc ttc tct acc 250
Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr
50 55 60 65
tat cct ctg gtt cca ggg cat gag att gtt ggt gaa gtg acg gaa gta 298
Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val
70 75 80
gga agc aat gta caa aaa ttc aaa gtt gga gac aga gtc ggt gtt gga 346
Gly Ser Asn Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly
85 90 95
tgc att gtg gga tct tgc cga tct tgt gaa aat tgt acc gac cac ctt 394
Cys Ile Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu
100 105 110
gag aac tac tgc ccc aaa cag ata ctc act tac ggt gcc aag tac tac 442
Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr
115 120 125
gac gga acc acc acc tat ggc ggt tac tct gac att atg gtg gcc gat 490
Asp Gly Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp
130 135 140 145
gaa cac ttc ata gta cgc atc cca gac aac ttg cct ctt gat ggt gct 538
Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala
150 155 160
gcg ccg ctc cta tgt gcc ggg att aca acc tac agc ccc ctg aga tat 586
Ala Pro Leu Leu Cys Ala Gly Ile Thr Tyr Ser Pro Leu Arg Tyr

165	170	175	
ttc gga ctt gac aag ccc ggc atg cat gta ggt gtg gtc ggc cta ggc Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly 180	185	190	634
ggt tta ggc cac gtc gcc gtg aag ttt gcc aag gct atg gga gtg aag Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys 195	200	205	682
gtt aca gtg att agt aca tcc cct aag aaa gag gag gaa gct cgt aaa Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Ala Arg Lys 210	215	220	730
cac cta gga gct gac tcg ttt ttg gtt agc cgt gac caa gat caa atg His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met 230	235	240	778
cag gct gcc att ggt acc atg gat ggg atc att gac acg gtt tct gca Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala 245	250	255	826
caa cat cct ctc ctg cct ttg att ggt ttg ttg aag tct cat gga aag Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys 260	265	270	874
ctt gtt atg gtt ggt gca cca gag aag cct ctt gaa ctg cca gtt ttt Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe 275	280	285	922
cct tta ctc atg gga aga aag atg gta gct ggt agc ggc att ggg ggt Pro Leu Leu Met Gly Arg Lys Met Val Ala Gly Ser Gly Ile Gly Gly 290	295	300	970
atg aag gag aca caa gag atg ata gat ttt gca gcc aag cac aac att Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Lys His Asn Ile 310	315	320	1018
aca gca gac atc gaa gtc ata cca atc gac tac ttg taacactgct Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu 325	330		1064
atggagcgtc tagtcaaagc agatgtcaga taccgttttgc tcatcgacat tggaaacaca ctgaaggcta gctcttaaat tctgcataatcc agactggatc aatgaagaaa caagaacaga aacggagact gattttagtgt catactcggt gttgggtttc cttgttagcat tttttgttgt ctgctacatg aataatgatc acatgaacaa ctgccttctg tgatgatttgc ataataaaag aatacatgaa caatgatact gccttctttt gtaatgtttt ttactatata atcatttcaa attatttgc tatatctcta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a			1124 1184 1244 1304 1364 1415
<210> 6 <211> 452 <212> PRT <213> <i>Fragaria x ananassa</i> <223> Strawberry alcohol acyl transferase			
<400> 6 Met Glu Lys Ile Glu Val Ser Ile Asn Ser Lys His Thr Ile Lys Pro			

1

5

10

15

Ser Thr Ser Ser Thr Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp
20 25 30

Gln Leu Thr Pro Pro Ala Tyr Val Pro Ile Val Phe Phe Tyr Pro Ile
35 40 45

Thr Asp His Asp Phe Asn Leu Pro Gln Thr Leu Ala Asp Leu Arg Gln
50 55 60

Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val
65 70 75 80

Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu
85 90 95

Glu Ala Arg Val Asn Cys Asp Met Thr Asp Phe Leu Arg Leu Arg Lys
100 105 110

Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu
115 120 125

Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Val
130 135 140

Phe Asp Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile
145 150 155 160

Asp Gly Gly Thr Ala Asp Cys Phe Leu Lys Ser Trp Gly Ala Val Phe
165 170 175

Arg Gly Cys Arg Glu Asn Ile Ile His Pro Ser Leu Ser Glu Ala Ala
180 185 190

Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Val Asp Gln
195 200 205

Met Glu Ala Leu Trp Phe Ala Gly Lys Val Ala Thr Arg Arg Phe
210 215 220

Val Phe Gly Val Lys Ala Ile Ser Ser Ile Gln Asp Glu Ala Lys Ser
225 230 235 240

Glu Ser Val Pro Lys Pro Ser Arg Val His Ala Val Thr Gly Phe Leu
245 250 255

Trp Lys His Leu Ile Ala Ala Ser Arg Ala Leu Thr Ser Gly Thr Thr
260 265 270

Ser Thr Arg Leu Ser Ile Ala Ala Gln Ala Val Asn Leu Arg Thr Arg
275 280 285

Met Asn Met Glu Thr Val Leu Asp Asn Ala Thr Gly Asn Leu Phe Trp
290 295 300

Trp Ala Gln Ala Ile Leu Glu Leu Ser His Thr Thr Pro Glu Ile Ser
305 310 315 320

Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys
325 330 335

Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Lys Gly Lys Glu Gly Tyr
 340 345 350
 Gly Arg Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
 355 360 365
 Glu Pro Ala Pro Asp Ile Tyr Leu Phe Ser Ser Trp Thr Asn Phe Phe
 370 375 380
 Asn Pro Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
 385 390 395 400
 Gly Lys Ile Glu Ser Ala Ser Cys Lys Phe Ile Ile Leu Val Pro Thr
 405 410 415
 Gln Cys Gly Ser Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Lys
 420 425 430
 Met Ala Met Leu Glu Gln Asp Pro His Phe Leu Ala Leu Ala Ser Pro
 435 440 445
 Lys Thr Leu Ile
 450

<210> 7
 <211> 663
 <212> DNA
 <213> Fragaria x ananassa

<220>
 <221> CDS
 <222> (3)..(545)
 <223> partial cdna

<220>
 <223> Strawberry alcohol dehydrogenase

<400> 7
 ag ttt ggt ctt gat gtg ggt gga tta agg gga ggg ata ttg gga ctt 47
 Phe Gly Leu Asp Val Gly Gly Leu Arg Gly Gly Ile Leu Gly Leu
 1 5 10 15
 gga ggt gtt gga cac atg ggg gtg aag ata gca aag gct atg gga cac 95
 Gly Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His
 20 25 30
 cat atc acc gtg ata agc tct tct gat aag aag aaa aaa gag gcc ttg 143
 His Ile Thr Val Ile Ser Ser Asp Lys Lys Lys Glu Ala Leu
 35 40 45
 gag cat att ggt gct gat gag tac ttg gtg agc tct gat gcc acc caa 191
 Glu His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln
 50 55 60
 atg caa gag gct atg gac tca ctg gat tac att att gac acc att cca 239
 Met Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro
 65 70 75
 gtg ttc cac cct ctt gag cct tac ctc tct ttg aag ctt gat ggg 287
 Val Phe His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly

80	85	90	95	
aag ttg atc ttg atg ggt gtt atc aac acc cca ttg caa ttt gtc tct				335
Lys Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser				
100	105	110		
cca ttg gtc atg ctt ggg gag gaa gac gat cac cgg gag ctt tgt ggg				383
Pro Leu Val Met Leu Gly Glu Glu Asp Asp His Arg Glu Leu Cys Gly				
115	120	125		
gag cat gaa gga gat gga gga gat gct cga gtt ctg caa aga gaa aga				431
Glu His Glu Gly Asp Gly Gly Asp Ala Arg Val Leu Gln Arg Glu Arg				
130	135	140		
gct gaa acg atg att gaa gtg gtg aag atg gac tac atc aac gaa gct				479
Ala Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala				
145	150	155		
ttc gaa agg ttg gag aag aac gac gtt agg tac agg ttc gtt gtg gat				527
Phe Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp				
160	165	170	175	
tgt tgc cgg cag caa tct tgatcaataa gaaagaaaaga aggcatcatc				575
Cys Cys Arg Gln Gln Ser				
180				
gagtgttgtc ctattttat cgagtactct gtctcatctt atcttaaaca atataaataa				635
acaaaagaaaa aaaaaaaaaa aaaaaaaaa				663
<210> 8				
<211> 694				
<212> DNA				
<213> Fragaria x ananassa				
<220>				
<221> CDS				
<222> (1)..(528)				
<223> partial cDNA				
<220>				
<223> Strawberry alcohol dehydrogenase				
<400> 8				
gtg cat tgc tat gcc tat gaa ggc aag atg caa gaa cat ctg caa tta				48
Val His Cys Tyr Ala Tyr Glu Gly Lys Met Gln Glu His Leu Gln Leu				
1	5	10	15	
tgt gaa gac gag ttt aaa aag ata atg aag ata aat ttc atg tct gca				96
Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala				
20	25	30		
tgg ttt ctg gta aat gcc gtt ggc aga aga atg cga gat cat aaa tca				144
Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser				
35	40	45		
gga ggt tcc atc ata ttg ttg acc tcg att gtt gga gct gaa aga ggg				192
Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly				
50	55	60		
ctt tat aca gga gct gtt gcc tat ggt gca tgt tcg gca gca ctg cag				240
Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln				

65	70	75	80	
cag tta gta agg tcg tcg gca ttg gag att gga aaa tac cag atc agg				288
Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg				
85	90	95		
gtt aat gca atc gca cgt ggt ttg cat ttg gaa gat gag ttt cct aag				336
Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys				
100	105	110		
tct gtg gga ata gag aga gca aag aag ctg gtg aat gat gca gtt ccg				384
Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro				
115	120	125		
ctg gag aga tgg ctt gat gtt aaa aat gat gtg gct tca agt gtc ata				432
Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile				
130	135	140		
tat ttg gtc agt gat ggt tca agg tac atg acg ggc aca act ata ttt				480
Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe				
145	150	155	160	
gtt gat ggg gca cag tct ctc gtg agg cct cga atg cgt tct tat atg				528
Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met				
165	170	175		
tgattcttgc tcctattata tcctccttagc cattattagc tacttaggtt tgttcataact 588				
tcataggtga actcattagc tattcttaca tttgttcctt atgaataaaag aagtcaagat 648				
tcaaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaa 694				
<210> 9				
<211> 1586				
<212> DNA				
<213> Fragaria x ananassa				
<220>				
<221> CDS				
<222> (78)..(1268)				
<223> cDNA				
<220>				
<223> Strawberry aminotransferase				
<400> 9				
aaaccgtcgg cgtctgtaaa tgcgtcgccg ctccggagaa gacagagttac aagactcagg 60				
tgaatcgcaa tgccaaatg gcc aag ctt caa gcc ggt tat ctt ttt cca 110				
Met Ala Lys Leu Gln Ala Gly Tyr Leu Phe Pro				
1	5	10		
gag att gcg agg agg aat gcg cac ttg cag aag cac cct gat gcg 158				
Glu Ile Ala Arg Arg Asn Ala His Leu Gln Lys His Pro Asp Ala				
15	20	25		
aag ata att cca ctt gga att ggt gat act acc gag cca att cca gaa 206				
Lys Ile Ile Pro Leu Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu				
30	35	40		
tat ata acc tct gca atg gca aag aga gca ctt gcc atg tcc acc cta 254				
Tyr Ile Thr Ser Ala Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu				

45	50	55	
gag ggt tac agt ggt tat gga cct gaa caa ggt gaa aag cca ctg aga			302
Glu Gly Tyr Ser Gly Tyr Gly Pro Glu Gln Gly Glu Lys Pro Leu Arg			
60	65	70	75
gtt gca att gct aaa acg ttt tat ggc gac ctt ggc ata gag gaa gat			350
Val Ala Ile Ala Lys Thr Phe Tyr Gly Asp Leu Gly Ile Glu Glu Asp			
80	85	90	
gac ata ttt gtt tct gat ggg gca aaa tgt gac ata tcc cgc ctt cag			398
Asp Ile Phe Val Ser Asp Gly Ala Lys Cys Asp Ile Ser Arg Leu Gln			
95	100	105	
gtt ctt ttt ggg gcg gat aaa aca ata gca gtg caa gat cca tcg tat			446
Val Leu Phe Gly Ala Asp Lys Thr Ile Ala Val Gln Asp Pro Ser Tyr			
110	115	120	
ccg gct tat gta gac tca agt gtt att atg ggc cag aca gga cag tat			494
Pro Ala Tyr Val Asp Ser Ser Val Ile Met Gly Gln Thr Gly Gln Tyr			
125	130	135	
cag aaa tct gtt cag aag ttt gga aac atc gag tac atg agg tgt act			542
Gln Lys Ser Val Gln Lys Phe Gly Asn Ile Glu Tyr Met Arg Cys Thr			
140	145	150	155
ccc gat aat gga ttt ttt cct gat ctg tcc tct act aag cga aca gat			590
Pro Asp Asn Gly Phe Phe Pro Asp Leu Ser Ser Thr Lys Arg Thr Asp			
160	165	170	
atc ata ttt ttc tgt tca cca aac aat cct act ggt tct tct gct gca aca			638
Ile Ile Phe Phe Cys Ser Pro Asn Asn Pro Thr Gly Ser Ala Ala Thr			
175	180	185	
agg gag caa ctg aca caa ctt gta aag ttt gcc aag gat aat ggt tca			686
Arg Glu Gln Leu Thr Gln Leu Val Lys Phe Ala Lys Asp Asn Gly Ser			
190	195	200	
atc ata gtc tat gat tct gca tat gcc atg tat atg tca gat gat aat			734
Ile Ile Val Tyr Asp Ser Ala Tyr Ala Met Tyr Met Ser Asp Asp Asn			
205	210	215	
cca cgc tcc atc ttt gaa atc cct gga gct aaa gat gtt gca ctt gag			782
Pro Arg Ser Ile Phe Glu Ile Pro Gly Ala Lys Asp Val Ala Leu Glu			
220	225	230	235
aca tca tca ttt agt aag tat gcc gga ttc act gga gtt cgt ttg ggg			830
Thr Ser Ser Phe Ser Lys Tyr Ala Gly Phe Thr Gly Val Arg Leu Gly			
240	245	250	
tgg act gtg gtt cca aag cag ttg cag tat tca gat ggt ttt caa gtt			878
Trp Thr Val Val Pro Lys Gln Leu Gln Tyr Ser Asp Gly Phe Gln Val			
255	260	265	
gcc aag gat ttc aac cgc att gtt tgt act tgc ttc aat ggt gca tcc			926
Ala Lys Asp Phe Asn Arg Ile Val Cys Thr Cys Phe Asn Gly Ala Ser			
270	275	280	
act att atc caa gct ggt ggt ctg gct tgc ctt caa cca aag ggt gtt			974
Thr Ile Ile Gln Ala Gly Gly Leu Ala Cys Leu Gln Pro Lys Gly Val			
285	290	295	

aag gct atg cac ggt gtg ata aat ttc tac aaa gaa aat act aag atc Lys Ala Met His Gly Val Ile Asn Phe Tyr Lys Glu Asn Thr Lys Ile 300 305 310 315	1022
ata atg gag acg ttt aac tct ctt ggc ttt aac gtg tat gga ggg aca Ile Met Glu Thr Phe Asn Ser Leu Gly Phe Asn Val Tyr Gly Thr 320 325 330	1070
aac gct cca tat gtg tgg gtc cac ttc cct gga caa agc tcc tgg gat Asn Ala Pro Tyr Val Trp Val His Phe Pro Gly Gln Ser Ser Trp Asp 335 340 345	1118
gtg ttt gct gag atc ctt gag aag act cat gtg gta acc aca cct gga Val Phe Ala Glu Ile Leu Glu Lys Thr His Val Val Thr Thr Pro Gly 350 355 360	1166
agt ggc ttt gga cct ggt ggt gaa ggt ttc atc agg gta agt gcc ttt Ser Gly Phe Gly Pro Gly Gly Glu Phe Ile Arg Val Ser Ala Phe 365 370 375	1214
gga cac agg aaa aat ata tta gaa gca tgt aaa aga ttc aag caa tta Gly His Arg Lys Asn Ile Leu Glu Ala Cys Lys Arg Phe Lys Gln Leu 380 385 390 395	1262
tac aag tgaggactgc ggatctgaat tgttagaccag tttctactgc atgctagttg Tyr Lys	1318
aacctatttg cctcccattt ccgttctatg ctaaatattt tagcacgttc caattccgta 1378	
ttcagtttgt cggctttagt ttatgaatta tggagatttt agctattgt aaaaatgattc 1438	
gatcagccctt gttttcatgt gttacactta attgttgaa catttggat gatcagaagc 1498	
tttgattctg tttgctagaa tagtataatt ttacctaaat aaagtggttg atctttcttg 1558	
gcctgcaaaa aaaaaaaaaa aaaaaaaaa 1586	
<210> 10	
<211> 1471	
<212> DNA	
<213> Cucumis melo	
<220>	
<221> CDS	
<222> (1)..(1368)	
<223> cDNA	
<220>	
<223> Honey dew melon alcohol acyl transferase	
<400> 10	
atg gac ttc tct ttt cac gta cga aaa tgc caa cca qaa ttg att gca Met Asp Phe Ser Phe His Val Arg Lys Cys Gln Pro Glu Leu Ile Ala 1 5 10 15	48
cca gca aat cct aca ccc tat gaa ttt aaa caa ctt tct gat gtg gat Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp 20 25 30	96
gat caa caa agc tta agg ctt caa ttg cca ttc gta aat atc tat ccc Asp Gln Gln Ser Leu Arg Leu Gln Leu Pro Phe Val Asn Ile Tyr Pro 35 40 45	144

cat aat cca agt ttg gag gga aga gat cca gtg aag gta ata aag gaa	192
His Asn Pro Ser Leu Glu Gly Arg Asp Pro Val Lys Val Ile Lys Glu	
50 55 60	
gca att gga aag gcg ttg gtg ttc tac tat cct tta gca gga aga ttg	240
Ala Ile Gly Lys Ala Leu Val Phe Tyr Tyr Pro Leu Ala Gly Arg Leu	
65 70 75 80	
aga gaa ggg cca ggt aga aag ctt ttt gtt gaa tgt aca ggt gaa gga	288
Arg Glu Gly Pro Gly Arg Lys Leu Phe Val Glu Cys Thr Gly Glu Gly	
85 90 95	
atc ttg ttt att gaa gcg gat gca gat gtg agc tta gaa gaa ttt tgg	336
Ile Leu Phe Ile Glu Ala Asp Ala Asp Val Ser Leu Glu Glu Phe Trp	
100 105 110	
gat act ctt cca tat tca ctt tca agc atg cag aac aat att ata cat	384
Asp Thr Leu Pro Tyr Ser Leu Ser Ser Met Gln Asn Asn Ile Ile His	
115 120 125	
aac gct tta aat tct gat gaa gtc ctc aat tct cca tta ttg ctc att	432
Asn Ala Leu Asn Ser Asp Glu Val Leu Asn Ser Pro Leu Leu Leu Ile	
130 135 140	
cag gtg aca cga ctc aag tgt gga ggt ttc att ttt ggt ctt tgt ttc	480
Gln Val Thr Arg Leu Lys Cys Gly Gly Phe Ile Phe Gly Leu Cys Phe	
145 150 155 160	
aat cat act atg gca gat ggt ttt ggt att gtc caa ttc atg aag gct	528
Asn His Thr Met Ala Asp Gly Phe Gly Ile Val Gln Phe Met Lys Ala	
165 170 175	
aca gcg gag ata gct cgt gga gct ttt gct cca tct att tta cca gta	576
Thr Ala Glu Ile Ala Arg Gly Ala Phe Ala Pro Ser Ile Leu Pro Val	
180 185 190	
tgg caa aga gct ctc tta acc gca aga gac cct ccc aga atc act ttt	624
Trp Gln Arg Ala Leu Leu Thr Ala Arg Asp Pro Pro Arg Ile Thr Phe	
195 200 205	
cgc cac tat gaa tac gac caa gta gtc gac atg aag agc ggc ctc att	672
Arg His Tyr Glu Tyr Asp Gln Val Val Asp Met Lys Ser Gly Leu Ile	
210 215 220	
cca gtc aat agc aag atc gat caa tta ttc ttc ttt agc caa ctt caa	720
Pro Val Asn Ser Lys Ile Asp Gln Leu Phe Phe Ser Gln Leu Gln	
225 230 235 240	
atc tcc acc ctt cgc caa act ttg cca gcc cac ctt cac gat tgc cct	768
Ile Ser Thr Leu Arg Gln Thr Leu Pro Ala His Leu His Asp Cys Pro	
245 250 255	
tcc ttc gag gtc ctc act gcc tat gtt tgg cgc ctc cgt acc ata gcc	816
Ser Phe Glu Val Leu Thr Ala Tyr Val Trp Arg Leu Arg Thr Ile Ala	
260 265 270	
ctt caa ttt aag cca gag gag gaa gtg cgg ttt ctt tgc gta atg aat	864
Leu Gln Phe Lys Pro Glu Glu Val Arg Phe Leu Cys Val Met Asn	
275 280 285	
cta cgc tcg aag atc gac ata cca tta ggg tat tat ggt aat gcg gta	912
Leu Arg Ser Lys Ile Asp Ile Pro Leu Gly Tyr Tyr Gly Asn Ala Val	

290	295	300	
gtt gtt cct gca gta atc acc acc gct gcg aag ctt tgt ggg aac cca			960
Val Val Pro Ala Val Ile Thr Thr Ala Ala Lys Leu Cys Gly Asn Pro			
305	310	315	320
ctt ggt tat gct gta gac ttg att agg aag gcc aag gct aag gca acg			1008
Leu Gly Tyr Ala Val Asp Leu Ile Arg Lys Ala Lys Ala Lys Ala Thr			
325	330	335	
atg gag tac ata aag tct acg gtg gat ctt atg gtg att aaa gga cga			1056
Met Glu Tyr Ile Lys Ser Thr Val Asp Leu Met Val Ile Lys Gly Arg			
340	345	350	
ccc tat ttc act gta gtt gga tca ttt atg atg tca gac cta acg aga			1104
Pro Tyr Phe Thr Val Val Gly Ser Phe Met Met Ser Asp Leu Thr Arg			
355	360	365	
att ggg gtt gaa aac gtg gac ttt gga tgg gga aag gcc att ttt gga			1152
Ile Gly Val Glu Asn Val Asp Phe Gly Trp Gly Lys Ala Ile Phe Gly			
370	375	380	
gga cct aca acc aca ggg gcc aga att aca cga ggt ttg gta agc ttt			1200
Gly Pro Thr Thr Gly Ala Arg Ile Thr Arg Gly Leu Val Ser Phe			
385	390	395	400
tgt gta cct ttc atg aat aga aat gga gaa aag gga act gcg tta agt			1248
Cys Val Pro Phe Met Asn Arg Asn Gly Glu Lys Gly Thr Ala Leu Ser			
405	410	415	
cta tgc ttg cct cct cca gcc atg gaa aga ttt agg gca aat gtt cat			1296
Leu Cys Leu Pro Pro Ala Met Glu Arg Phe Arg Ala Asn Val His			
420	425	430	
gcc tcg ttg caa gtg aaa caa gtg gtt gat gca gtt gat agc cat atg			1344
Ala Ser Leu Gln Val Lys Gln Val Val Asp Ala Val Asp Ser His Met			
435	440	445	
caa act att caa tct gct tcg aaa taaataatat tgttgaaggt gggctctgagt			1398
Gln Thr Ile Gln Ser Ala Ser Lys			
450	455		
tgactcgacc atatcgatgc atgcaagctt gatccggctg ctaacaaagc ccgaaaggaa			1458
gctgagttgc tgt			1471
<210> 11			
<211> 1485			
<212> DNA			
<213> Malus sp.			
<220>			
<221> CDS			
<222> (1)..(1362)			
<223> cDNA			
<220>			
<223> Apple alcohol acyl transferase			
<400> 11			
atg tca ttc tca gta ctt cag gtg aaa cga ttg caa ccg gaa ctt ata			48
Met Ser Phe Ser Val Leu Gln Val Lys Arg Leu Gln Pro Glu Leu Ile			

1

5

10

15

act	ccg	gca	aag	tca	acg	cct	caa	gaa	aca	aag	ttt	ctc	tca	gat	att	96
Thr	Pro	Ala	Lys	Ser	Thr	Pro	Gln	Glu	Thr	Lys	Phe	Leu	Ser	Asp	Ile	
															20	
															25	
															30	
gac	gac	caa	gaa	agc	ttg	aga	gtt	cag	att	cca	atc	ata	atg	tgt	tac	144
Asp	Asp	Gln	Glu	Ser	Leu	Arg	Val	Gln	Ile	Pro	Ile	Ile	Met	Cys	Tyr	
															35	
															40	
															45	
aaa	gac	aac	cct	tca	ctt	aat	aaa	aat	cgt	aat	ccc	gtt	aag	gca	att	192
Lys	Asp	Asn	Pro	Ser	Leu	Asn	Lys	Asn	Arg	Asn	Pro	Val	Lys	Ala	Ile	
															50	
															55	
															60	
agg	gaa	gcc	tta	agt	aga	gca	tta	gtg	tat	tac	tac	ccc	tta	gct	gga	240
Arg	Glu	Ala	Leu	Ser	Arg	Ala	Leu	Val	Tyr	Tyr	Tyr	Tyr	Pro	Leu	Gly	
															65	
															70	
															75	
															80	
agg	ctt	agg	gaa	ggg	cct	aat	aga	aag	ctc	gtg	gtc	gat	tgc	aat	ggt	288
Arg	Leu	Arg	Glu	Gly	Pro	Asn	Arg	Lys	Leu	Val	Val	Asp	Cys	Asn	Gly	
															85	
															90	
															95	
gaa	ggt	atc	ttg	ttc	gtt	gag	gct	tct	gct	gat	gtc	aca	ctt	gag	caa	336
Glu	Gly	Ile	Leu	Phe	Val	Glu	Ala	Ser	Ala	Asp	Val	Thr	Leu	Glu	Gln	
															100	
															105	
															110	
cta	gga	gac	aaa	att	cta	ccc	cct	tgt	cca	ctt	tta	gag	gag	ttc	tta	384
Leu	Gly	Asp	Lys	Ile	Leu	Pro	Pro	Cys	Pro	Leu	Leu	Glu	Glu	Phe	Leu	
															115	
															120	
															125	
tat	aat	ttt	cca	ggc	tct	gat	gga	att	att	gat	tgt	cct	ttg	ctg	ctg	432
Tyr	Asn	Phe	Pro	Gly	Ser	Asp	Gly	Ile	Ile	Asp	Cys	Pro	Leu	Leu	Leu	
															130	
															135	
															140	
att	cag	gtg	acc	tgt	ctt	aca	tgt	gga	ggt	ttc	ata	ctt	gca	ttg	cgc	480
Ile	Gln	Val	Thr	Cys	Leu	Thr	Cys	Gly	Gly	Phe	Ile	Leu	Ala	Leu	Arg	
															145	
															150	
															155	
															160	
cta	aac	cac	aca	atg	tgt	gat	gca	gct	gga	ttg	ctc	ttg	ttc	ctg	acc	528
Leu	Asn	His	Thr	Met	Cys	Asp	Ala	Ala	Gly	Leu	Leu	Leu	Phe	Leu	Thr	
															165	
															170	
															175	
gcc	atc	gcg	gag	atg	gca	aga	ggc	gca	cat	gca	cca	tct	att	cta	cca	576
Ala	Ile	Ala	Glu	Met	Ala	Arg	Gly	Ala	His	Ala	Pro	Ser	Ile	Leu	Pro	
															180	
															185	
															190	
gtg	tgg	gag	aga	gag	ctc	ttg	ttc	gct	cga	gat	cca	cca	aga	att	aca	624
Val	Trp	Glu	Arg	Glu	Leu	Leu	Phe	Ala	Arg	Asp	Pro	Pro	Arg	Ile	Thr	
															195	
															200	
															205	
tgt	gct	cgt	cat	gaa	tat	gaa	gac	gtg	att	ggt	cat	tct	gat	ggc	tca	672
Cys	Ala	Arg	His	Glu	Tyr	Glu	Asp	Val	Ile	Gly	His	Ser	Asp	Gly	Ser	
															210	
															215	
															220	
tac	gca	tcc	agt	aac	cag	tca	aac	atg	gtt	caa	cga	tct	ttc	tac	ttt	720
Tyr	Ala	Ser	Ser	Asn	Gln	Ser	Asn	Met	Val	Gln	Arg	Ser	Phe	Tyr	Phe	
															225	
															230	
															235	
															240	
ggt	gcc	aag	gag	atg	aga	gtc	ctt	cga	aaa	cag	att	cca	ccc	cac	cta	768
Gly	Ala	Lys	Glu	Met	Arg	Val	Leu	Arg	Lys	Gln	Ile	Pro	Pro	His	Leu	
															245	
															250	
															255	

att tcc act tgc tcc aca ttt gac ttg atc aca gct tgt ttg tgg aaa Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys 260 265 270	816
tgt cgc act ctt gca ctt aac att aat cca aaa gag gct gtt cga gtt Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val 275 280 285	864
tca tgc att gtc aat gca cga gga aag cac aac aat gta cgt ctt ccc Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro 290 295 300	912
ttg gga tac tat ggc aat gca ttt gca ttt cca gct gca att tcg aag Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys 305 310 315 320	960
gct gaa cct cta tgc aaa aat cca ctg gga tat gct ttg gag ttg gtc Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val 325 330 335	1008
aag aag gct aaa gct acc atg aat gaa gaa tac tta aga tca gtg gca Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala 340 345 350	1056
gat ctt ttg gta cta aga ggg cga cct caa tat tca tcg aca gga agt Asp Leu Leu Val Leu Arg Gly Arg Pro Gln Tyr Ser Ser Thr Gly Ser 355 360 365	1104
tat tta ata gtt tct gat aat acg cgt gta ggt ttt gga gat gtc aat Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn 370 375 380	1152
ttt gga tgg gga cag ccg gta ttt gct gga ccc gtc aag gcc ttg gat Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp 385 390 395 400	1200
ttg att agc ttc tac gtt caa cac aaa aac aac aca gag gat gga ata Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile 405 410 415	1248
ttg gta cca atg tgt ttg cca tcc tcg gcc atg gag aga ttt cag cag Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln 420 425 430	1296
gaa cta gag agg att act cag gaa cct aag gag gat ata tgt aac aac Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn 435 440 445	1344
ctt aga tca act agt caa tgatgttaagt gttaaacgta atgcactttc Leu Arg Ser Thr Ser Gln 450	1392
tgtaatgttag agttgtgtct cttggaaacctt atcncaagag ttatagctgt tatccaaagg	1452
tctgaatgtt attaaaaaat agccaataat aag	1485
<210> 12	
<211> 1291	
<212> DNA	
<213> Musa sp.	
<220>	

<221> CDS
<222> (1)..(1257)
<223> cDNA

<220>
<223> Banana alcohol acyl transferase

<400> 12
atg agc ttc gct gtg acc aga aca agc cgg tct ttg gtc act cca tgc 48
Met Ser Phe Ala Val Thr Arg Thr Ser Arg Ser Leu Val Thr Pro Cys
1 5 10 15

ggg gtc acg ccg acg ggc tcg ctc ggc ctc tcc gcc atc gac cgg gtg 96
Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val
20 25 30

ccc ggc ctc agg cat atg gtg cgg tcg cta cac gtg ttc agg caa ggc 144
Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly
35 40 45

cgg gag ccg gcc agg atc atc agg gaa gca ctg tcg aag gcg ctg gtg 192
Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val
50 55 60

aag tac tac ccc ttc gcg ggg cgg ttc gtg gac gat ccc gag ggc ggc 240
Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly
65 70 75 80

ggc gag gtt cgt gtc gct tgc act ggc gag ggc gct tgg ttc gtc gag 288
Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu
85 90 95

gcc aag gcg gac tgc agc ttg gag gac gtg aag tac ctc gat ctc ccg 336
Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro
100 105 110

ctc atg atc cct gag gac gcg ctc ctg ccc aag ccc tgc ccg gga ctg 384
Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu
115 120 125

aac ccc ctc gac ctc cct ctc atg ctg cag gtg aca gag ttc gtg ggc 432
Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly
130 135 140

ggc gga ttc gtg gtc ggc ctc atc tcc gtc cat acc atc gcc gac ggc 480
Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly
145 150 155 160

ctc ggc gtc gtc cag ttc atc aac gcc gtc gcc gag atc gcc cgt ggc 528
Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly
165 170 175

ctg ccg aag ccc acc gtg gag cct gca tgg tcc cgg gag gtc ata ccc 576
Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro
180 185 190

aac cca cct aag ctg cct ccc ggt ggc ccc gtg ttc ccc tcc ttc 624
Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe
195 200 205

aag ctg ctc cac gcc acc gtc gac cta tcc cct gac cac atc gat cac 672
Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His

210	215	220	
gtc aag tcc cga cac ttg gag ctc acc ggc cag cgc tgc tct acc ttc			720
Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe			
225	230	235	240
gac gtc gcc atc gcc aac ctg tgg cag tcc cgc acg cgc gcc atc aac			768
Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn			
245	250	255	
ctg gac cca ggc gtc gac gtg cac gtg tgc ttc ttc gcc aac act cgc			816
Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg			
260	265	270	
cac ctg ttg cgc cag gtc gtc ctc ctg ccc ccc gag gat ggc tac tac			864
His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr			
275	280	285	
ggc aac tgc ttc tac ccg gtg acc gcc acc cca agc ggc agg atc			912
Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile			
290	295	300	
gca tcg gcc gag ctc atc gat gtc gtc agc atc atc agg gac gcc aag			960
Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys			
305	310	315	320
tcg agg ctg ccg ggc gag ttc gcc aag tgg gct gcc ggg gat ttc aag			1008
Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys			
325	330	335	
gac gac cct tac gag ctc agc ttc acg tac aac tcg ctg ttc gtg tcg			1056
Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser			
340	345	350	
gac tgg acc ccg ctc ggc ttc ctc gac gtc gac tac ggc tgg ggc aag			1104
Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys			
355	360	365	
ccc ctc cac gtt ata ccg ttc gcg tac ttg gac atc atg gcg gtc ggc			1152
Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly			
370	375	380	
atc atc ggg gcg ccg ccg gcg cca aag ggg act cgg gtg atg gcg			1200
Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala			
385	390	395	400
cag tgc gtc gag aag gag cac atg cag gcg ttc ctg gaa gag atg aaa			1248
Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys			
405	410	415	
ggc ttc gct taaaccagca gcagtgtagt acttgtcagt atcc			1291
Gly Phe Ala			

<210> 13
 <211> 1488
 <212> DNA
 <213> Fragaria vesca

 <220>
 <221> CDS
 <222> (1)..(1365)
 <223> cDNA

<220>

<223> Strawberry vesca alcohol acyl transferase

<400> 13

atg gag aaa att gag gtc agt ata att tcc aaa cac acc atc aaa cca Met Glu Lys Ile Glu Val Ser Ile Ile Ser Lys His Thr Ile Lys Pro	48
1 5 10 15	
tca act tcc tct tca cca ctt cag cct tac aag ctt acc ctg ctc gac Ser Thr Ser Ser Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp	96
20 25 30	
cag ctc act cct cca tcg tat gtc ccc atg gta ttc ttc tac ccc att Gln Leu Thr Pro Pro Ser Tyr Val Pro Met Val Phe Phe Tyr Pro Ile	144
35 40 45	
act ggc cct gca gtc ttc aat ctt caa acc cta gct gac tta aga cat Thr Gly Pro Ala Val Phe Asn Leu Gln Thr Leu Ala Asp Leu Arg His	192
50 55 60	
gcc ctt tcc gag act ctc act ttg tac tat cca ctc tct gga agg gtc Ala Leu Ser Glu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val	240
65 70 75 80	
aaa aac aac cta tac atc gat gat ttt gaa gag ggt gtc cca tac ctt Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu	288
85 90 95	
gag gct cga gtg aac tgt gac atg aat gat ttt cta agg ctt ccg aaa Glu Ala Arg Val Asn Cys Asp Met Asn Asp Phe Leu Arg Leu Pro Lys	336
100 105 110	
atc gag tgc cta aat gag ttt gtt cca ata aaa cca ttt agt atg gaa Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu	384
115 120 125	
gca ata tct gat gag cgt tac cct ttg ctc gga gtt caa gtt aac att Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Ile	432
130 135 140	
ttc aac tcc gga ata gca atc ggg gtc tcc gtc tct cac aag ctc atc Phe Asn Ser Gly Ile Ala Ile Gly Val Ser Val His Lys Leu Ile	480
145 150 155 160	
gat gga aga act tca gac tgt ttt ctc aag tcg tgg tgt gct gtt ttt Asp Gly Arg Thr Ser Asp Cys Phe Leu Lys Ser Trp Cys Ala Val Phe	528
165 170 175	
cgt ggt tct cgt gac aaa atc ata cat cct aat ctc tct caa gca gca Arg Gly Ser Arg Asp Lys Ile Ile His Pro Asn Leu Ser Gln Ala Ala	576
180 185 190	
ttg ctt ttc cca cca aga gat gac ttg cct gaa aag tat gcc cgt cag Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Ala Arg Gln	624
195 200 205	
atg gaa ggg tta tgg ttt gtc gga aaa aaa gtt gct aca agg aga ttt Met Glu Gly Leu Trp Phe Val Gly Lys Lys Val Ala Thr Arg Arg Phe	672
210 215 220	
gta ttt ggt gcg aaa gcc ata tct gta att caa gat gaa gca aag agc Val Phe Gly Ala Lys Ala Ile Ser Val Ile Gln Asp Glu Ala Lys Ser	720

225	230	235	240	
gag tcc gtg ccc aag cca tca cga gtt cag gct gtc act agt ttt ctc Glu Ser Val Pro Lys Pro Ser Arg Val Gln Ala Val Thr Ser Phe Leu 245 250 255				768
tgg aaa cat cta atc gct act tct cggtt gca cta aca tca ggt act act Trp Lys His Leu Ile Ala Thr Ser Arg Ala Leu Thr Ser Gly Thr Thr 260 265 270				816
tca aca aga ctt tct ata gca acc cag gta gtg aac ata aga tca cgg Ser Thr Arg Leu Ser Ile Ala Thr Gln Val Val Asn Ile Arg Ser Arg 275 280 285				864
agg aac atg gag aca gtg tgg gat aat gcc att gga aac ttg ata tgg Arg Asn Met Glu Thr Val Trp Asp Asn Ala Ile Gly Asn Leu Ile Trp 290 295 300				912
ttc gct ccg gcc ata cta gag cta agt cat aca aca cta gag atc agt Phe Ala Pro Ala Ile Leu Glu Leu Ser His Thr Thr Leu Glu Ile Ser 305 310 315 320				960
gat ctt aag ctg tgt gac ttg gtt aac ttg ctc aat gga tct gtc aaa Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys 325 330 335				1008
caa tgt aac ggt gat tac ttt gag act ttc atg ggt aaa gag gga tat Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Met Gly Lys Glu Gly Tyr 340 345 350				1056
gga agc atg tgc gag tat cta gat ttt cag agg act atg agt tct atg Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met 355 360 365				1104
gaa cca gca cca gag att tat tta ttc acg agc tgg act aat ttt ttc Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp Thr Asn Phe Phe 370 375 380				1152
aac caa ctt gat ttt gga tgg ggg agg aca tca tgg att gga gtt gca Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala 385 390 395 400				1200
gga aaa att gaa tct gca ttt tgc aat ctc aca aca tta gtt cca aca Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr 405 410 415				1248
cca tgc gat act gga att gaa gcg tgg gtg aat cta gaa gaa gaa aaa Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Lys 420 425 430				1296
atg gct atg cta gaa caa gat ccc cag ttt cta gca cta gca tct cca Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro 435 440 445				1344
aag acg cta att tca aga tat tgattaagga agattatgcg gctcgtgcaa Lys Thr Leu Ile Ser Arg Tyr 450 455				1395
tgtttccatt ttgttgtat taaggcttaa attagttcac cagccaatca ataagatgca agtatgatag actcggtcta cgtatgttat ccg				1455 1488

<210> 14
 <211> 434
 <212> PRT
 <213> Citrus limon
 <223> Citrus limon alcohol acyl transferase

<400> 14
 Met Lys Ile His Val Lys Glu Ser Thr Ile Ile Arg Pro Ala Gln Glu
 1 5 10 15

Thr Pro Lys His Arg Leu Gln Ile Ser Asp Leu Asp Met Ile Val Pro
 20 25 30

Ser Asn Tyr Val Pro Ser Val Tyr Phe Tyr Arg Arg Ser Ser Asp Cys
 35 40 45

Thr Asp Phe Phe Glu Val Gly Leu Leu Lys Lys Ala Leu Ser Glu Val
 50 55 60

Leu Val Pro Phe Tyr Pro Val Ala Gly Arg Leu Gln Lys Asp Glu Asn
 65 70 75 80

Arg Lys Ile Glu Ile Leu Cys Asn Gly Glu Gly Val Leu Phe Leu Glu
 85 90 95

Ala Glu Thr Ser Cys Gly Ile Asp Asp Phe Gly Asp Phe Ser Gln Gly
 100 105 110

Ser Lys Leu Leu Thr Leu Val Pro Thr Val Gly Asp Thr Lys Asp Ile
 115 120 125

Ser Ser His Pro Leu Leu Met Ala Gln Val Thr Tyr Phe Lys Cys Gly
 130 135 140

Gly Val Cys Val Gly Thr Arg Val Asn His Thr Leu Val Asp Gly Ala
 145 150 155 160

Ser Ala Tyr His Ile Ile Asn Ser Trp Ala Glu Thr Thr Arg Gly Val
 165 170 175

Pro Ile Ser Thr Gln Pro Phe Tyr Asp Arg Thr Ile Leu Ser Val Gly
 180 185 190

Val Pro Thr Ser Pro Lys Phe His His Ile Glu Tyr Asp Pro Pro Pro
 195 200 205

Ser Met Asn Ala Pro Pro Thr Gln Asn Pro Glu Ile Ile Ser Thr Ala
 210 215 220

Ile Leu Asn Leu Ser Leu Asp Gln Ile His Thr Leu Lys Glu Lys Ser
 225 230 235 240

Lys Thr Asp His Glu Pro Asn Val Lys Tyr Ser Arg Met Ala Ile Leu
 245 250 255

Ala Ala His Ile Trp Arg Ser Met Cys Lys Ala Arg Gly Leu Ser Asp
 260 265 270

Asp Gln Val Ser Lys Leu His Phe Pro Thr Asp Gly Arg Gln Arg Leu
 275 280 285

Asn Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Thr

290

295

300

Ser Leu Thr Ala Ser Ser Gly Asp Ile Leu Ser Glu Pro Leu Asn His
305 310 315 320

Thr Val Glu Arg Ile Gln Lys Ala Leu Lys Arg Met Asp Asp Glu Tyr
325 330 335

Leu Lys Ser Ala Leu Ala Tyr Leu Lys Gln Gln Pro Asp Leu Asn Ala
340 345 350

Leu Arg Lys Gly Gly His Ile Tyr Lys Cys Pro Asn Leu Asn Ile Val
355 360 365

Asn Leu Ala Asn Met Pro Met Tyr Val Ala Asn Phe Gly Trp Gly Gln
370 375 380

Pro Ile Phe Ala Arg Ile Val Asn Thr Tyr Tyr Glu Gly Ile Ala His
385 390 395 400

Ile Tyr Pro Ser Pro Ser Asn Asp Gly Thr Leu Ser Val Val Ile Asn
405 410 415

Ser Val Ala Asp His Met Gln Leu Phe Lys Lys Phe Phe Tyr Glu Ile
420 425 430

Phe Asp

<210> 15

<211> 1296

<212> DNA

<213> Mangifera indica

<220>

<221> CDS

<222> (1)..(1293)

<223> cDNA

<220>

<223> Mango alcohol acyl transferase

<400> 15

atg ata atc acg gtg aag gag tcg acg atg gtc ccg ccg tcg gcg gag 48
Met Ile Ile Thr Val Lys Glu Ser Thr Met Val Pro Pro Ser Ala Glu
1 5 10 15

acg ccg agg ata tct ctg tgg aac tcc aac gcc gat ctg gtg gtt ccc 96
Thr Pro Arg Ile Ser Leu Trp Asn Ser Asn Ala Asp Leu Val Val Pro
20 25 30

cga ttt cat act ccc agc gtt tac ttc tac cgg ccc acc ggg gcc ata 144
Arg Phe His Thr Pro Ser Val Tyr Phe Tyr Arg Pro Thr Gly Ala Ile
35 40 45

aac ttc ttt gat ggt aag ttg ctc aag gag gct ctc ggc aag gct ctg 192
Asn Phe Phe Asp Gly Lys Leu Leu Lys Glu Ala Leu Gly Lys Ala Leu
50 55 60

gtg ccg ttc tac cca atg gcg ggg cgg tta aag cgt gac gaa gat gga 240
Val Pro Phe Tyr Pro Met Ala Gly Arg Leu Lys Arg Asp Glu Asp Gly
65 70 75 80

agg att gag atc gat tgt aat gct gaa ggc gtc ttg ttt gtt gag gcc Arg Ile Glu Ile Asp Cys Asn Ala Glu Gly Val Leu Phe Val Glu Ala 85 90 95	288
gaa act ccc tct gtt att gat gat ttt ggt gac ttt gcg ccc act tta Glu Thr Pro Ser Val Ile Asp Asp Phe Gly Asp Phe Ala Pro Thr Leu 100 105 110	336
gag ctc aag cag ctc att ccg aca gtg gat tac tcc ggc ggg atc tct Glu Leu Lys Gln Leu Ile Pro Thr Val Asp Tyr Ser Gly Gly Ile Ser 115 120 125	384
acg tat ccc cta ttg gcg tta cag gtt act cac ttc aaa tgt ggt gga Thr Tyr Pro Leu Leu Ala Leu Gln Val Thr His Phe Lys Cys Gly Gly 130 135 140	432
gtt tca ctt ggt gta ggt atg caa cac cat gcg gca gat gga ttt tct Val Ser Leu Gly Val Gly Met Gln His His Ala Ala Asp Gly Phe Ser 145 150 155 160	480
ggt ctt cac ttt gta aac aca tgg tca gac att gct cgt ggt ctt gat Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp 165 170 175	528
gtt aac atc acc ctg ttc att gac cgg act ctg ctc aga gca cag gat Val Asn Ile Thr Leu Phe Ile Asp Arg Thr Leu Leu Arg Ala Gln Asp 180 185 190	576
ccc cct cag cct act ttc cca cac aca tgg aat acc agg ccc cct cct Pro Pro Gln Pro Thr Phe Pro His Thr Trp Asn Thr Arg Pro Pro Pro 195 200 205	624
tcc ctg aaa act cct cca cca gca gtt tct gag cct act gct gtc tcc Ser Leu Lys Thr Pro Pro Pro Ala Val Ser Glu Pro Thr Ala Val Ser 210 215 220	672
att ttt aag ttg acg cgg gac cag ctc aac atc ctc aaa gcc aag gcc Ile Phe Lys Leu Thr Arg Asp Gln Leu Asn Ile Leu Lys Ala Lys Ala 225 230 235 240	720
aaa gaa gat ggt aac act atc aac tat agc tca tat gag atg ctg gcg Lys Glu Asp Gly Asn Thr Ile Asn Tyr Ser Ser Tyr Glu Met Leu Ala 245 250 255	768
ggt cat gtc tgg aga tct gca tgc aag gca cgc ggc tta tct gat gat Gly His Val Trp Arg Ser Ala Cys Lys Ala Arg Gly Leu Ser Asp Asp 260 265 270	816
caa gag act aaa ttg tac ata gca act gac gga cgt gct aga tta atc Gln Glu Thr Lys Leu Tyr Ile Ala Thr Asp Gly Arg Ala Arg Leu Ile 275 280 285	864
ccc cca ctt cca cct ggt tac ttt ggg aat gtg ata ttt aca gcc aca Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Ala Thr 290 295 300	912
cca atg gca gta gca ggt gat ctc cag tca aag cct ata tgg tat gct Pro Met Ala Val Ala Gly Asp Leu Gln Ser Lys Pro Ile Trp Tyr Ala 305 310 315 320	960
gct ggc cag att cat gat gcc ttg gtt cga atg gac aac gac tat tta Ala Gly Gln Ile His Asp Ala Leu Val Arg Met Asp Asn Asp Tyr Leu	1008

325	330	335	
agg tca gcc ctc gat tac cta gag ctt cag cct gat tta tca gca tta Arg Ser Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Ala Leu 340	345	350	1056
gtt cgt ggt gcc cat aca ttt agg tgt cca aat ctc ggg att act agt Val Arg Gly Ala His Thr Phe Arg Cys Pro Asn Leu Gly Ile Thr Ser 355	360	365	1104
tgg gtt aga ctg cca ata cat gat gca gat ttt ggt tgg ggt cca ccc Trp Val Arg Leu Pro Ile His Asp Ala Asp Phe Gly Trp Gly Pro Pro 370	375	380	1152
aca ttt atg ggg cct ggt ggg att gca tat gaa ggc tta tca ttt gta Thr Phe Met Gly Pro Gly Ile Ala Tyr Glu Gly Leu Ser Phe Val 385	390	395	1200
ttg cca agc cct aca aat gat ggg agc tta tca gtt gcc atc tct cta Leu Pro Ser Pro Thr Asn Asp Gly Ser Leu Ser Val Ala Ile Ser Leu 405	410	415	1248
caa tct gaa cac atg aaa ctg ttt cag aag ttc ttt tat gat att taa Gln Ser Glu His Met Lys Leu Phe Gln Lys Phe Phe Tyr Asp Ile 420	425	430	1296
<p><210> 16</p> <p><211> 1436</p> <p><212> DNA</p> <p><213> Citrus limon</p>			
<p><220></p> <p><221> CDS</p> <p><222> (34)..(1311)</p> <p><223> cDNA</p>			
<p><220></p> <p><223> Lemon acyl transferase</p>			
<p><400> 16</p> <p>atcccacacta ataattcttt catatgatcg ggg atg gat ctc caa atc acc tgc Met Asp Leu Gln Ile Thr Cys 1 5</p>			
<p>acc gaa atc atc aag cct tct tcg ccg acg cct caa cac caa agt acc Thr Glu Ile Ile Lys Pro Ser Ser Pro Thr Pro Gln His Gln Ser Thr 10 15 20</p>			
<p>tat aaa ctt tca att att gat caa tta act cct aat gtt tac ttt tcc Tyr Lys Leu Ser Ile Ile Asp Gln Leu Thr Pro Asn Val Tyr Phe Ser 25 30 35</p>			
<p>atc att ctc ttg tat tca aaa gct ggt gaa agt acc gcc aaa act tca Ile Ile Leu Leu Tyr Ser Lys Ala Gly Glu Ser Thr Ala Lys Thr Ser 40 45 50 55</p>			
<p>gat cac ctc aaa gaa tct ctt tca aat aca tta acc cac tac tat cct Asp His Leu Lys Glu Ser Leu Ser Asn Thr Leu Thr His Tyr Tyr Pro 60 65 70</p>			
<p>tta gct ggg caa ctc aaa tat gat caa ctt att gtt gat tgt aac gac Leu Ala Gly Gln Leu Lys Tyr Asp Gln Leu Ile Val Asp Cys Asn Asp</p>			

75	80	85	
caa ggt gtc ccg ttc atc gaa gca cac gtc acc aac gac atg cgt cag Gln Gly Val Pro Phe Ile Glu Ala His Val Thr Asn Asp Met Arg Gln 90 95 100			342
ctt ctt aaa ata cca aat att gat gtt ctc gaa caa ctc cta cca ttc Leu Leu Lys Ile Pro Asn Ile Asp Val Leu Glu Gln Leu Leu Pro Phe 105 110 115			390
aaa ccg cat gag ggt ttt gat tct gat cgt tcc aac cta acc gtt cag Lys Pro His Glu Gly Phe Asp Ser Asp Arg Ser Asn Leu Thr Val Gln 120 125 130 135			438
gtc aat tac ttt ggt tgt gaa gga atg gcg att ggt ctg tgc ttc aga Val Asn Tyr Phe Gly Cys Glu Gly Met Ala Ile Gly Leu Cys Phe Arg 140 145 150			486
cac aaa gtt att gat gca aca acg gct gca ttc ttt gtt aag aac tgg His Lys Val Ile Asp Ala Thr Thr Ala Ala Phe Phe Val Lys Asn Trp 155 160 165			534
ggg gta att gct cgt ggt gct gga gaa att aag gac gtc atc att gat Gly Val Ile Ala Arg Gly Ala Gly Glu Ile Lys Asp Val Ile Ile Asp 170 175 180			582
cat gct tcc ctg ttt ccc gca aga gat tta tcg tgc tta aca aag agt His Ala Ser Leu Phe Pro Ala Arg Asp Leu Ser Cys Leu Thr Lys Ser 185 190 195			630
gtt gac gaa gag ttt ttg aag cca gag tct gaa aca aag cgc ttt gtg Val Asp Glu Glu Phe Leu Lys Pro Glu Ser Glu Thr Lys Arg Phe Val 200 205 210 215			678
ttt gat ggt gcc act ata gct tct tta caa gaa acg ttt gca agt ttt Phe Asp Gly Ala Thr Ile Ala Ser Leu Gln Glu Thr Phe Ala Ser Phe 220 225 230			726
gaa cga cgt cca aca cgc ttt gag gtt gtc tca gca gtt att ttg ggt Glu Arg Arg Pro Thr Arg Phe Glu Val Val Ser Ala Val Ile Leu Gly 235 240 245			774
gct ttg ata act gca acg aga gaa tct gat gat gag tct aac gtt cct Ala Leu Ile Thr Ala Thr Arg Glu Ser Asp Asp Glu Ser Asn Val Pro 250 255 260			822
gaa cgt ttg gac acg ata att tca gtc aat cta cgg cag aga atg aat Glu Arg Leu Asp Thr Ile Ile Ser Val Asn Leu Arg Gln Arg Met Asn 265 270 275			870
cca cca ttc ccg gag cat tgc atg ggg aat ata ata tcc ggg gga tta Pro Pro Phe Pro Glu His Cys Met Gly Asn Ile Ile Ser Gly Gly Leu 280 285 290 295			918
gtg tat tgg cca ctg gag aaa aaa gtt gat tac ggg tgt tta gca aaa Val Tyr Trp Pro Leu Glu Lys Lys Val Asp Tyr Gly Cys Leu Ala Lys 300 305 310			966
gag att cat gaa tca ata aag aaa gtg gac gat caa ttt gtc agg aag Glu Ile His Glu Ser Ile Lys Lys Val Asp Asp Gln Phe Ala Arg Lys 315 320 325			1014

ttc tat ggg gac gca gag ttc ttg aac ctg ccg agg ctt gcg ggt gct Phe Tyr Gly Asp Ala Glu Phe Leu Asn Leu Pro Arg Leu Ala Gly Ala 330 335 340	1062
gag gat gtg aag aag cgg gag ttt tgg gtt act agt tgg tgc aaa act Glu Asp Val Lys Lys Arg Glu Phe Trp Val Thr Ser Trp Cys Lys Thr 345 350 355	1110
ccg ctg tat gaa gct gat ttc ggg tgg ggg aat cct aag tgg gca ggc Pro Leu Tyr Glu Ala Asp Phe Gly Trp Gly Asn Pro Lys Trp Ala Gly 360 365 370 375	1158
aac tcc atg agg ctt aat cag att act gtt ttc ttt gac agt agt gat Asn Ser Met Arg Leu Asn Gln Ile Thr Val Phe Phe Asp Ser Ser Asp 380 385 390	1206
ggt gag gga gtt gaa gct tgg gtg ggg ttg ccc aga aaa gac atg gct Gly Glu Gly Val Glu Ala Trp Val Gly Leu Pro Arg Lys Asp Met Ala 395 400 405	1254
cga ttt gaa aaa gat tct ggc atc ctt gct tac act tcc cct aat cca Arg Phe Glu Lys Asp Ser Gly Ile Leu Ala Tyr Thr Ser Pro Asn Pro 410 415 420	1302
agc ata ttt tgagggtta tttatTTTTT attgcactgt ttgttatttg Ser Ile Phe 425	1351
tactggcttg ctggaaacat attctggcaa atttcgctga tgcaagtatc attctccata aaaatgtcaa aaaaaaaaaa aaaaaa	1411 1436
<210> 17 <211> 1648 <212> DNA <213> Citrus limon	
<220> <221> CDS <222> (52)..(1524) <223> cDNA	
<220> <223> Lemon acyl transferase	
<400> 17 gctaggctgg ctttcattta gcttccatct ctttctctct gtcaataact c atg gct 57 Met Ala 1	
gca att gaa aac aga gta aca cta aag aag cat gag gtt acc aaa gtc 105 Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr Lys Val 5 10 15	
acc cct ttc gtc aac ccc aac tca aag acg acg tcg ttt act ctc gat 153 Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr Leu Asp 20 25 30	
ctc acc tat ttc gac ttt ttc tgg aag aat cct cct gtg gaa cgc 201 Leu Thr Tyr Phe Asp Phe Phe Trp Phe Lys Asn Pro Pro Val Glu Arg 35 40 45 50	

ctc ttc ttc tat gag atg act gac ttg acg tgg gat tta ttc aac tcg Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe Asn Ser 55 60 65	249
gag atc ctc cca aag ctg aag cac tcc ctt tcc ttc act ctc ctt cat Glu Ile Leu Pro Lys Leu Lys His Ser Leu Ser Phe Thr Leu Leu His 70 75 80	297
tac ctc cct ctt gct ggt cac atc atg tgg ccg ctg gat gcc gca aag Tyr Leu Pro Leu Ala Gly His Ile Met Trp Pro Leu Asp Ala Ala Lys 85 90 95	345
cct gcc gtc tac tac ttt ccc gac caa aac gac ggc gtt tca ttc gca Pro Ala Val Tyr Tyr Phe Pro Asp Gln Asn Asp Gly Val Ser Phe Ala 100 105 110	393
gtt gct gag tgg tct tcc gag tgc cac gca ggc ttc cat cac ctc tcc Val Ala Glu Trp Ser Ser Glu Cys His Ala Gly Phe His His Leu Ser 115 120 125 130	441
ggc aac gga atc cgc caa gca gtt gaa ttt cat cct ctt gtg ccc cag Gly Asn Gly Ile Arg Gln Ala Val Glu Phe His Pro Leu Val Pro Gln 135 140 145	489
ttg tcg ctt acg gac gat aaa gct gag gta att gcc atc caa ata aca Leu Ser Leu Thr Asp Asp Lys Ala Glu Val Ile Ala Ile Gln Ile Thr 150 155 160	537
ctg ttt ccg aat caa ggc ttc tca att ggt gtt tca tct cac cat gca Leu Phe Pro Asn Gln Gly Phe Ser Ile Gly Val Ser Ser His His Ala 165 170 175	585
att ctt gat gga aaa act tcg acc ttg ttc ctg aaa tct tgg gct tat Ile Leu Asp Gly Lys Thr Ser Thr Leu Phe Leu Lys Ser Trp Ala Tyr 180 185 190	633
ttg tgc aaa caa tta caa tta tgc cat cac cct tgt ttg tca cct gaa Leu Cys Lys Gln Leu Gln Leu Cys His His Pro Cys Leu Ser Pro Glu 195 200 205 210	681
cta acc cct ctt ctc gac cgg act gtc atc aaa gat ccg aca ggt cag Leu Thr Pro Leu Leu Asp Arg Thr Val Ile Lys Asp Pro Thr Gly Gln 215 220 225	729
gac atg ctg caa ctg aat aag tgg gtt gtc ggg tcg gat aat tcg gat Asp Met Leu Gln Leu Asn Lys Trp Val Val Gly Ser Asp Asn Ser Asp 230 235 240	777
ccc cag aag ata cgg agc ttg aag gtt tta cca ttc tta gac tct gag Pro Gln Lys Ile Arg Ser Leu Lys Val Leu Pro Phe Leu Asp Ser Glu 245 250 255	825
tct ctg aac aaa ttg gtc cga gcc aca ttt gag ttg acg cgt gaa gat Ser Leu Asn Lys Leu Val Arg Ala Thr Phe Glu Leu Thr Arg Glu Asp 260 265 270	873
att acg aaa ctc agg cac aag gtt aat cat cag tta tca aaa tca tca Ile Thr Lys Leu Arg His Lys Val Asn His Gln Leu Ser Lys Ser Ser 275 280 285 290	921
aaa tca aag caa gtt cgt tta tca act ttt gtg ctt aca tta gct tat Lys Ser Lys Gln Val Arg Leu Ser Thr Phe Val Leu Thr Leu Ala Tyr	969

295	300	305	
gtg ttt gtt tgc atg gct aaa gct aaa tta gcc aaa gcc aaa act gaa Val Phe Val Cys Met Ala Lys Ala Lys Leu Ala Lys Ala Lys Thr Glu 310	315	320	1017
gct gaa gct gca gca ggt aat gat gaa att aaa aat att att gtg gga Ala Glu Ala Ala Gly Asn Asp Glu Ile Lys Asn Ile Ile Val Gly 325	330	335	1065
ttc act gcg gat tat agg agc cgt ttg gat cct cca att cca ctt aat Phe Thr Ala Asp Tyr Arg Ser Arg Leu Asp Pro Pro Ile Pro Leu Asn 340	345	350	1113
tat ttt ggt aac tgc aat ggg aga cat tgt gag act gca aaa gca agt Tyr Phe Gly Asn Cys Asn Gly Arg His Cys Glu Thr Ala Lys Ala Ser 355	360	365	1161
gat ttc gtt caa gaa aat ggg gtt gct ttt gtt gca gag atg tta agt Asp Phe Val Gln Glu Asn Gly Val Ala Phe Val Ala Glu Met Leu Ser 375	380	385	1209
gat atg gtc aaa ggg atc gat gcg gat gcc att gaa gcc aat gat gat Asp Met Val Lys Gly Ile Asp Ala Asp Ala Ile Glu Ala Asn Asp Asp 390	395	400	1257
aag gtt tca gaa ata ttg gaa att ctg aaa gaa gga gca atg att ttt Lys Val Ser Glu Ile Leu Glu Ile Leu Lys Glu Gly Ala Met Ile Phe 405	410	415	1305
tct gtg gct ggc tcg acc caa ttt gat gtt tac ggg tcg gat ttc ggg Ser Val Ala Gly Ser Thr Gln Phe Asp Val Tyr Gly Ser Asp Phe Gly 420	425	430	1353
tgg ggg agg ccc aag aag gtg gag att gtg tca ata gat agg aca caa Trp Gly Arg Pro Lys Lys Val Glu Ile Val Ser Ile Asp Arg Thr Gln 435	440	445	1401
gcc atc tct ttg gca gag aga aga gat gga gga ggc ggc gtt gag gtt Ala Ile Ser Leu Ala Glu Arg Arg Asp Gly Gly Gly Val Glu Val 455	460	465	1449
gga gtt gtt tta gag aag caa caa atg gag gtt ttt gaa tct gta ttt Gly Val Val Leu Glu Lys Gln Gln Met Glu Val Phe Glu Ser Val Phe 470	475	480	1497
gct gat gga ctg aaa aat gat ctt gtt taattatgtatgtatcatct Ala Asp Gly Leu Lys Asn Asp Leu Val 485	490		1544
aaatttctca atatattattt ggtcatattc aaaagaaata aattattgcg gatttttgtg accaccaaataaaaataactcttttggaaaa aaaaaaaaaaaa aaaa			1604 1648
<210> 18			
<211> 1520			
<212> DNA			
<213> Citrus limon			
<220>			
<221> CDS			
<222> (4)...(1344)			

<223> cDNA

<220>

<223> Lemon acyl transferase

<400> 18

aac atg gca gca agc tca ctg cat ggc aaa gaa gct aca gtt ata tat	48
Met Ala Ala Ser Ser Leu His Gly Lys Glu Ala Thr Val Ile Tyr	
1 5 10 15	
cct tct gag cca acc cca tct acg gtt ttg tct ctc tca gct ctt gat	96
Pro Ser Glu Pro Thr Pro Ser Thr Val Leu Ser Leu Ser Ala Leu Asp	
20 25 30	
tct cag ctt ttc ttg cgt ttc act att gag tat ctc ttg gtc tat aga	144
Ser Gln Leu Phe Leu Arg Phe Thr Ile Glu Tyr Leu Leu Val Tyr Arg	
35 40 45	
cct cgc cct ggt ttg gac cca ctt gct acc gtg gct cgt gtc aag tcc	192
Pro Arg Pro Gly Leu Asp Pro Leu Ala Thr Val Ala Arg Val Lys Ser	
50 55 60	
gca ctc gcc aaa gcc ttg gtt cct tac tat ccc ctc gcg ggt cgg gtc	240
Ala Leu Ala Lys Ala Leu Val Pro Tyr Tyr Pro Leu Ala Gly Arg Val	
65 70 75	
aga gct aaa caa gac ggg tcg ggc tta ttg gaa gtc gtg tgt cta ggc	288
Arg Ala Lys Gln Asp Gly Ser Gly Leu Leu Glu Val Val Cys Leu Gly	
80 85 90 95	
caa ggc gct gtg ttc atc gaa gcc gtc gac cgt gaa agt acg atc acc	336
Gln Gly Ala Val Phe Ile Glu Ala Val Asp Arg Glu Ser Thr Ile Thr	
100 105 110	
gat ttt gag agt gct ccc agg tat gtt act cag tgg agg aaa ctg ctg	384
Asp Phe Glu Ser Ala Pro Arg Tyr Val Thr Gln Trp Arg Lys Leu Leu	
115 120 125	
tgc tta tac gtg gcg gat gtt ctc aaa ggg gcc cca cct ctt gtc gtt	432
Ser Leu Tyr Val Ala Asp Val Leu Lys Gly Ala Pro Pro Leu Val Val	
130 135 140	
cag ctg act tgg ctt aga gat gga gcc gca gcg ctc ggt att ggc ttt	480
Gln Leu Thr Trp Leu Arg Asp Gly Ala Ala Leu Gly Ile Gly Phe	
145 150 155	
aac cat tgt gtt tgc gat ggt atc ggc agc gcc gag ttc ctc aac ttg	528
Asn His Cys Val Cys Asp Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu	
160 165 170 175	
ttt act gag tta tgt acg agc cgt cat aac gaa ctg ggt ggt ggc cat	576
Phe Thr Glu Leu Cys Thr Ser Arg His Asn Glu Leu Gly Gly His	
180 185 190	
tct ctg ccg aaa ccc gtt tgg gat cgc cac cta atg aac tcc tcc tca	624
Ser Leu Pro Lys Pro Val Trp Asp Arg His Leu Met Asn Ser Ser Ser	
195 200 205	
tca cgt caa cag cat gca gat aca cgt gcc agc tca gtg agt cac ctg	672
Ser Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu	
210 215 220	

gaa ttc aac aga gtg gct gat ctt tgt ggt ttt gtt tct cgt ttt tcc Glu Phe Asn Arg Val Ala Asp Leu Cys Gly Phe Val Ser Arg Phe Ser 225 230 235	720
aac gaa agg ctt gtt ccc act tca ata acg ttc gat aaa cga cgc tta Asn Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu 240 245 250 255	768
aac gag ctg cgg aag ctg gct ctg tcc acg agt cga ccc agt gag ctg Asn Glu Leu Arg Lys Leu Ala Leu Ser Thr Ser Arg Pro Ser Glu Leu 260 265 270	816
gct tac acg tca ttt gaa gtt ctt tca gct cat gtg tgg aga agc tgg Ala Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp 275 280 285	864
gct agg tcg ttg aat ctt ccg tcg aat caa atc ttg aag ctt cta ttt Ala Arg Ser Leu Asn Leu Pro Ser Asn Gln Ile Leu Lys Leu Leu Phe 290 295 300	912
agc atc aat gta cgt aac cgt gtc aag ccg agt ctc ccc agt ggc tat Ser Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr 305 310 315	960
tat ggc gat gca ttt gta tta ggc tgt gct caa acg agg gtt aaa gat Tyr Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp 320 325 330 335	1008
ttg aca gag aag gac tta ggg cat gca gca atg ttg gtt aaa aag gcg Leu Thr Glu Lys Asp Leu Gly His Ala Ala Met Leu Val Lys Lys Ala 340 345 350	1056
aaa gag aga gtt gat agt gag tat gtg aag tcg gtc atc gac tca gtg Lys Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val 355 360 365	1104
agt cac acg aga gcg tgt ccc gac tca gtc ggg gtg ttg ata gtg tcg Ser His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser 370 375 380	1152
cag tgg tca agg cta ggg tta gag aga gtt gac ttt ggg atg ggg agg Gln Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg 385 390 395	1200
ccg act caa gtg ggt ccc att tgc tgc gac agg tat tgc ctg ttt cta Pro Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu 400 405 410 415	1248
ccg gtt ttc aat cag acg gac gct gtt aag gtg atg gtg gcg gtc ccc Pro Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro 420 425 430	1296
aca agt gca gtt gac aag tat gag cat ctc gcg aag ggc tta tgc tgg Thr Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp 435 440 445	1344
tgaggaccac accgcatgat gacccacca tgtaatacgt tgacttataa actcagttt 1404	
acttttaact ttttaacaa gtgatgaaat ttcaatgtt gactcatcac ttgtatcctg 1464	
atccaataaa taattgaatt gagttcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1520	

<210> 19
 <211> 455
 <212> PRT
 <213> Fragaria vesca
 <223> Strawberry vesca alcohol acyl transferase

<400> 19
 Met Glu Lys Ile Glu Val Ser Ile Ile Ser Lys His Thr Ile Lys Pro
 1 5 10 15

Ser Thr Ser Ser Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp
 20 25 30

Gln Leu Thr Pro Pro Ser Tyr Val Pro Met Val Phe Phe Tyr Pro Ile
 35 40 45

Thr Gly Pro Ala Val Phe Asn Leu Gln Thr Leu Ala Asp Leu Arg His
 50 55 60

Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val
 65 70 75 80

Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu
 85 90 95

Glu Ala Arg Val Asn Cys Asp Met Asn Asp Phe Leu Arg Leu Pro Lys
 100 105 110

Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu
 115 120 125

Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Ile
 130 135 140

Phe Asn Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile
 145 150 155 160

Asp Gly Arg Thr Ser Asp Cys Phe Leu Lys Ser Trp Cys Ala Val Phe
 165 170 175

Arg Gly Ser Arg Asp Lys Ile Ile His Pro Asn Leu Ser Gln Ala Ala
 180 185 190

Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Ala Arg Gln
 195 200 205

Met Glu Gly Leu Trp Phe Val Gly Lys Lys Val Ala Thr Arg Arg Phe
 210 215 220

Val Phe Gly Ala Lys Ala Ile Ser Val Ile Gln Asp Glu Ala Lys Ser
 225 230 235 240

Glu Ser Val Pro Lys Pro Ser Arg Val Gln Ala Val Thr Ser Phe Leu
 245 250 255

Trp Lys His Leu Ile Ala Thr Ser Arg Ala Leu Thr Ser Gly Thr Thr
 260 265 270

Ser Thr Arg Leu Ser Ile Ala Thr Gln Val Val Asn Ile Arg Ser Arg
 275 280 285

Arg Asn Met Glu Thr Val Trp Asp Asn Ala Ile Gly Asn Leu Ile Trp

290	295	300
Phe Ala Pro Ala Ile Leu Glu Leu Ser His	Thr Thr Leu Glu Ile Ser	
305	310	315
Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys		
325	330	335
Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Met Gly Lys Glu Gly Tyr		
340	345	350
Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met		
355	360	365
Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp Thr Asn Phe Phe		
370	375	380
Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala		
385	390	395
Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr		
405	410	415
Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Lys		
420	425	430
Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro		
435	440	445
Lys Thr Leu Ile Ser Arg Tyr		
450	455	
<210> 20		
<211> 419		
<212> PRT		
<213> Musa sp.		
<223> Banana alcohol acyl transferase		
<400> 20		
Met Ser Phe Ala Val Thr Arg Thr Ser Arg Ser Leu Val Thr Pro Cys		
1	5	10
Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val		
20	25	30
Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly		
35	40	45
Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val		
50	55	60
Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly		
65	70	75
80		
Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu		
85	90	95
Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro		
100	105	110
Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu		
115	120	125

Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly
 130 135 140
 Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly
 145 150 155 160
 Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly
 165 170 175
 Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro
 180 185 190
 Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe
 195 200 205
 Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His
 210 215 220
 Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe
 225 230 235 240
 Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn
 245 250 255
 Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg
 260 265 270
 His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr
 275 280 285
 Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile
 290 295 300
 Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys
 305 310 315 320
 Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys
 325 330 335
 Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser
 340 345 350
 Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys
 355 360 365
 Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly
 370 375 380
 Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala
 385 390 395 400
 Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys
 405 410 415
 Gly Phe Ala
 <210> 21
 <211> 454
 <212> PRT
 <213> Malus sp.
 <223> Apple alcohol acyl transferase

<400> 21
 Met Ser Phe Ser Val Leu Gln Val Lys Arg Leu Gln Pro Glu Leu Ile
 1 5 10 15
 Thr Pro Ala Lys Ser Thr Pro Gln Glu Thr Lys Phe Leu Ser Asp Ile
 20 25 30
 Asp Asp Gln Glu Ser Leu Arg Val Gln Ile Pro Ile Ile Met Cys Tyr
 35 40 45
 Lys Asp Asn Pro Ser Leu Asn Lys Asn Arg Asn Pro Val Lys Ala Ile
 50 55 60
 Arg Glu Ala Leu Ser Arg Ala Leu Val Tyr Tyr Tyr Pro Leu Ala Gly
 65 70 75 80
 Arg Leu Arg Glu Gly Pro Asn Arg Lys Leu Val Val Asp Cys Asn Gly
 85 90 95
 Glu Gly Ile Leu Phe Val Glu Ala Ser Ala Asp Val Thr Leu Glu Gln
 100 105 110
 Leu Gly Asp Lys Ile Leu Pro Pro Cys Pro Leu Leu Glu Glu Phe Leu
 115 120 125
 Tyr Asn Phe Pro Gly Ser Asp Gly Ile Ile Asp Cys Pro Leu Leu Leu
 130 135 140
 Ile Gln Val Thr Cys Leu Thr Cys Gly Gly Phe Ile Leu Ala Leu Arg
 145 150 155 160
 Leu Asn His Thr Met Cys Asp Ala Ala Gly Leu Leu Leu Phe Leu Thr
 165 170 175
 Ala Ile Ala Glu Met Ala Arg Gly Ala His Ala Pro Ser Ile Leu Pro
 180 185 190
 Val Trp Glu Arg Glu Leu Leu Phe Ala Arg Asp Pro Pro Arg Ile Thr
 195 200 205
 Cys Ala Arg His Glu Tyr Glu Asp Val Ile Gly His Ser Asp Gly Ser
 210 215 220
 Tyr Ala Ser Ser Asn Gln Ser Asn Met Val Gln Arg Ser Phe Tyr Phe
 225 230 235 240
 Gly Ala Lys Glu Met Arg Val Leu Arg Lys Gln Ile Pro Pro His Leu
 245 250 255
 Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys
 260 265 270
 Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val
 275 280 285
 Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro
 290 295 300
 Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys
 305 310 315 320
 Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val

325	330	335
Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala		
340	345	350
Asp Leu Leu Val Leu Arg Gly Arg Pro Gln Tyr Ser Ser Thr Gly Ser		
355	360	365
Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn		
370	375	380
Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp		
385	390	395
Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile		
405	410	415
Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln		
420	425	430
Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn		
435	440	445
Leu Arg Ser Thr Ser Gln		
450		
<210> 22		
<211> 431		
<212> PRT		
<213> Mangifera indica		
<223> Mango alcohol acyl transferase		
<400> 22		
Met Ile Ile Thr Val Lys Glu Ser Thr Met Val Pro Pro Ser Ala Glu		
1	5	10
15		
Thr Pro Arg Ile Ser Leu Trp Asn Ser Asn Ala Asp Leu Val Val Pro		
20	25	30
Arg Phe His Thr Pro Ser Val Tyr Phe Tyr Arg Pro Thr Gly Ala Ile		
35	40	45
Asn Phe Phe Asp Gly Lys Leu Leu Lys Glu Ala Leu Gly Lys Ala Leu		
50	55	60
Val Pro Phe Tyr Pro Met Ala Gly Arg Leu Lys Arg Asp Glu Asp Gly		
65	70	75
80		
Arg Ile Glu Ile Asp Cys Asn Ala Glu Gly Val Leu Phe Val Glu Ala		
85	90	95
Glu Thr Pro Ser Val Ile Asp Asp Phe Gly Asp Phe Ala Pro Thr Leu		
100	105	110
Glu Leu Lys Gln Leu Ile Pro Thr Val Asp Tyr Ser Gly Gly Ile Ser		
115	120	125
Thr Tyr Pro Leu Leu Ala Leu Gln Val Thr His Phe Lys Cys Gly Gly		
130	135	140
Val Ser Leu Gly Val Gly Met Gln His His Ala Ala Asp Gly Phe Ser		
145	150	155
160		

Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp
 165 170 175
 Val Asn Ile Thr Leu Phe Ile Asp Arg Thr Leu Leu Arg Ala Gln Asp
 180 185 190
 Pro Pro Gln Pro Thr Phe Pro His Thr Trp Asn Thr Arg Pro Pro Pro
 195 200 205
 Ser Leu Lys Thr Pro Pro Ala Val Ser Glu Pro Thr Ala Val Ser
 210 215 220
 Ile Phe Lys Leu Thr Arg Asp Gln Leu Asn Ile Leu Lys Ala Lys Ala
 225 230 235 240
 Lys Glu Asp Gly Asn Thr Ile Asn Tyr Ser Ser Tyr Glu Met Leu Ala
 245 250 255
 Gly His Val Trp Arg Ser Ala Cys Lys Ala Arg Gly Leu Ser Asp Asp
 260 265 270
 Gln Glu Thr Lys Leu Tyr Ile Ala Thr Asp Gly Arg Ala Arg Leu Ile
 275 280 285
 Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Ala Thr
 290 295 300
 Pro Met Ala Val Ala Gly Asp Leu Gln Ser Lys Pro Ile Trp Tyr Ala
 305 310 315 320
 Ala Gly Gln Ile His Asp Ala Leu Val Arg Met Asp Asn Asp Tyr Leu
 325 330 335
 Arg Ser Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Ala Leu
 340 345 350
 Val Arg Gly Ala His Thr Phe Arg Cys Pro Asn Leu Gly Ile Thr Ser
 355 360 365
 Trp Val Arg Leu Pro Ile His Asp Ala Asp Phe Gly Trp Gly Pro Pro
 370 375 380
 Thr Phe Met Gly Pro Gly Gly Ile Ala Tyr Glu Gly Leu Ser Phe Val
 385 390 395 400
 Leu Pro Ser Pro Thr Asn Asp Gly Ser Leu Ser Val Ala Ile Ser Leu
 405 410 415
 Gln Ser Glu His Met Lys Leu Phe Gln Lys Phe Phe Tyr Asp Ile
 420 425 430
 <210> 23
 <211> 426
 <212> PRT
 <213> Citrus limon
 <223> Lemon acyl transferase
 <400> 23
 Met Asp Leu Gln Ile Thr Cys Thr Glu Ile Ile Lys Pro Ser Ser Pro
 1 5 10 15
 Thr Pro Gln His Gln Ser Thr Tyr Lys Leu Ser Ile Ile Asp Gln Leu

20

25

30

Thr Pro Asn Val Tyr Phe Ser Ile Ile Leu Leu Tyr Ser Lys Ala Gly
 35 40 45

Glu Ser Thr Ala Lys Thr Ser Asp His Leu Lys Glu Ser Leu Ser Asn
 50 55 60

Thr Leu Thr His Tyr Tyr Pro Leu Ala Gly Gln Leu Lys Tyr Asp Gln
 65 70 75 80

Leu Ile Val Asp Cys Asn Asp Gln Gly Val Pro Phe Ile Glu Ala His
 85 90 95

Val Thr Asn Asp Met Arg Gln Leu Leu Lys Ile Pro Asn Ile Asp Val
 100 105 110

Leu Glu Gln Leu Leu Pro Phe Lys Pro His Glu Gly Phe Asp Ser Asp
 115 120 125

Arg Ser Asn Leu Thr Val Gln Val Asn Tyr Phe Gly Cys Glu Gly Met
 130 135 140

Ala Ile Gly Leu Cys Phe Arg His Lys Val Ile Asp Ala Thr Thr Ala
 145 150 155 160

Ala Phe Phe Val Lys Asn Trp Gly Val Ile Ala Arg Gly Ala Gly Glu
 165 170 175

Ile Lys Asp Val Ile Ile Asp His Ala Ser Leu Phe Pro Ala Arg Asp
 180 185 190

Leu Ser Cys Leu Thr Lys Ser Val Asp Glu Glu Phe Leu Lys Pro Glu
 195 200 205

Ser Glu Thr Lys Arg Phe Val Phe Asp Gly Ala Thr Ile Ala Ser Leu
 210 215 220

Gln Glu Thr Phe Ala Ser Phe Glu Arg Arg Pro Thr Arg Phe Glu Val
 225 230 235 240

Val Ser Ala Val Ile Leu Gly Ala Leu Ile Thr Ala Thr Arg Glu Ser
 245 250 255

Asp Asp Glu Ser Asn Val Pro Glu Arg Leu Asp Thr Ile Ile Ser Val
 260 265 270

Asn Leu Arg Gln Arg Met Asn Pro Pro Phe Pro Glu His Cys Met Gly
 275 280 285

Asn Ile Ile Ser Gly Gly Leu Val Tyr Trp Pro Leu Glu Lys Lys Val
 290 295 300

Asp Tyr Gly Cys Leu Ala Lys Glu Ile His Glu Ser Ile Lys Lys Val
 305 310 315 320

Asp Asp Gln Phe Ala Arg Lys Phe Tyr Gly Asp Ala Glu Phe Leu Asn
 325 330 335

Leu Pro Arg Leu Ala Gly Ala Glu Asp Val Lys Lys Arg Glu Phe Trp
 340 345 350

Val Thr Ser Trp Cys Lys Thr Pro Leu Tyr Glu Ala Asp Phe Gly Trp
 355 360 365
 Gly Asn Pro Lys Trp Ala Gly Asn Ser Met Arg Leu Asn Gln Ile Thr
 370 375 380
 Val Phe Phe Asp Ser Ser Asp Gly Glu Gly Val Glu Ala Trp Val Gly
 385 390 395 400
 Leu Pro Arg Lys Asp Met Ala Arg Phe Glu Lys Asp Ser Gly Ile Leu
 405 410 415
 Ala Tyr Thr Ser Pro Asn Pro Ser Ile Phe
 420 425
 <210> 24
 <211> 491
 <212> PRT
 <213> Citrus limon
 <223> Lemon acyl transferase
 <400> 24
 Met Ala Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr
 1 5 10 15
 Lys Val Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr
 20 25 30
 Leu Asp Leu Thr Tyr Phe Asp Phe Phe Trp Phe Lys Asn Pro Pro Val
 35 40 45
 Glu Arg Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe
 50 55 60
 Asn Ser Glu Ile Leu Pro Lys Leu Lys His Ser Leu Ser Phe Thr Leu
 65 70 75 80
 Leu His Tyr Leu Pro Leu Ala Gly His Ile Met Trp Pro Leu Asp Ala
 85 90 95
 Ala Lys Pro Ala Val Tyr Tyr Phe Pro Asp Gln Asn Asp Gly Val Ser
 100 105 110
 Phe Ala Val Ala Glu Trp Ser Ser Glu Cys His Ala Gly Phe His His
 115 120 125
 Leu Ser Gly Asn Gly Ile Arg Gln Ala Val Glu Phe His Pro Leu Val
 130 135 140
 Pro Gln Leu Ser Leu Thr Asp Asp Lys Ala Glu Val Ile Ala Ile Gln
 145 150 155 160
 Ile Thr Leu Phe Pro Asn Gln Gly Phe Ser Ile Gly Val Ser Ser His
 165 170 175
 His Ala Ile Leu Asp Gly Lys Thr Ser Thr Leu Phe Leu Lys Ser Trp
 180 185 190
 Ala Tyr Leu Cys Lys Gln Leu Gln Leu Cys His His Pro Cys Leu Ser
 195 200 205
 Pro Glu Leu Thr Pro Leu Leu Asp Arg Thr Val Ile Lys Asp Pro Thr

210	215	220
Gly Gln Asp Met Leu Gln Leu Asn Lys Trp Val Val Gly Ser Asp Asn		
225	230	235
Ser Asp Pro Gln Lys Ile Arg Ser Leu Lys Val Leu Pro Phe Leu Asp		
245	250	255
Ser Glu Ser Leu Asn Lys Leu Val Arg Ala Thr Phe Glu Leu Thr Arg		
260	265	270
Glu Asp Ile Thr Lys Leu Arg His Lys Val Asn His Gln Leu Ser Lys		
275	280	285
Ser Ser Lys Ser Lys Gln Val Arg Leu Ser Thr Phe Val Leu Thr Leu		
290	295	300
Ala Tyr Val Phe Val Cys Met Ala Lys Ala Lys Leu Ala Lys Ala Lys		
305	310	315
Thr Glu Ala Glu Ala Ala Gly Asn Asp Glu Ile Lys Asn Ile Ile		
325	330	335
Val Gly Phe Thr Ala Asp Tyr Arg Ser Arg Leu Asp Pro Pro Ile Pro		
340	345	350
Leu Asn Tyr Phe Gly Asn Cys Asn Gly Arg His Cys Glu Thr Ala Lys		
355	360	365
Ala Ser Asp Phe Val Gln Glu Asn Gly Val Ala Phe Val Ala Glu Met		
370	375	380
Leu Ser Asp Met Val Lys Gly Ile Asp Ala Asp Ala Ile Glu Ala Asn		
385	390	395
Asp Asp Lys Val Ser Glu Ile Leu Glu Ile Leu Lys Glu Gly Ala Met		
405	410	415
Ile Phe Ser Val Ala Gly Ser Thr Gln Phe Asp Val Tyr Gly Ser Asp		
420	425	430
Phe Gly Trp Gly Arg Pro Lys Lys Val Glu Ile Val Ser Ile Asp Arg		
435	440	445
Thr Gln Ala Ile Ser Leu Ala Glu Arg Arg Asp Gly Gly Gly Val		
450	455	460
Glu Val Gly Val Val Leu Glu Lys Gln Gln Met Glu Val Phe Glu Ser		
465	470	475
Val Phe Ala Asp Gly Leu Lys Asn Asp Leu Val		
485	490	
<210> 25		
<211> 447		
<212> PRT		
<213> Citrus limon		
<223> Lemon acyl transferase		
<400> 25		
Met Ala Ala Ser Ser Leu His Gly Lys Glu Ala Thr Val Ile Tyr Pro		
1	5	10
15		

Ser Glu Pro Thr Pro Ser Thr Val Leu Ser Leu Ser Ala Leu Asp Ser
 20 25 30
 Gln Leu Phe Leu Arg Phe Thr Ile Glu Tyr Leu Leu Val Tyr Arg Pro
 35 40 45
 Arg Pro Gly Leu Asp Pro Leu Ala Thr Val Ala Arg Val Lys Ser Ala
 50 55 60
 Leu Ala Lys Ala Leu Val Pro Tyr Tyr Pro Leu Ala Gly Arg Val Arg
 65 70 75 80
 Ala Lys Gln Asp Gly Ser Gly Leu Leu Glu Val Val Cys Leu Gly Gln
 85 90 95
 Gly Ala Val Phe Ile Glu Ala Val Asp Arg Glu Ser Thr Ile Thr Asp
 100 105 110
 Phe Glu Ser Ala Pro Arg Tyr Val Thr Gln Trp Arg Lys Leu Leu Ser
 115 120 125
 Leu Tyr Val Ala Asp Val Leu Lys Gly Ala Pro Pro Leu Val Val Gln
 130 135 140
 Leu Thr Trp Leu Arg Asp Gly Ala Ala Ala Leu Gly Ile Gly Phe Asn
 145 150 155 160
 His Cys Val Cys Asp Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu Phe
 165 170 175
 Thr Glu Leu Cys Thr Ser Arg His Asn Glu Leu Gly Gly His Ser
 180 185 190
 Leu Pro Lys Pro Val Trp Asp Arg His Leu Met Asn Ser Ser Ser Ser
 195 200 205
 Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu Glu
 210 215 220
 Phe Asn Arg Val Ala Asp Leu Cys Gly Phe Val Ser Arg Phe Ser Asn
 225 230 235 240
 Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu Asn
 245 250 255
 Glu Leu Arg Lys Leu Ala Leu Ser Thr Ser Arg Pro Ser Glu Leu Ala
 260 265 270
 Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp Ala
 275 280 285
 Arg Ser Leu Asn Leu Pro Ser Asn Gln Ile Leu Lys Leu Leu Phe Ser
 290 295 300
 Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr Tyr
 305 310 315 320
 Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp Leu
 325 330 335
 Thr Glu Lys Asp Leu Gly His Ala Ala Met Leu Val Lys Lys Ala Lys
 340 345 350

Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val Ser
 355 360 365
 His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser Gln
 370 375 380
 Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg Pro
 385 390 395 400
 Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu Pro
 405 410 415
 Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro Thr
 420 425 430
 Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp
 435 440 445
 <210> 26
 <211> 456
 <212> PRT
 <213> Cucumis melo
 <223> Honey dew melon alcohol acyl transferase
 <400> 26
 Met Asp Phe Ser Phe His Val Arg Lys Cys Gln Pro Glu Leu Ile Ala
 1 5 10 15
 Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp
 20 25 30
 Asp Gln Gln Ser Leu Arg Leu Gln Leu Pro Phe Val Asn Ile Tyr Pro
 35 40 45
 His Asn Pro Ser Leu Glu Gly Arg Asp Pro Val Lys Val Ile Lys Glu
 50 55 60
 Ala Ile Gly Lys Ala Leu Val Phe Tyr Tyr Pro Leu Ala Gly Arg Leu
 65 70 75 80
 Arg Glu Gly Pro Gly Arg Lys Leu Phe Val Glu Cys Thr Gly Glu Gly
 85 90 95
 Ile Leu Phe Ile Glu Ala Asp Ala Asp Val Ser Leu Glu Glu Phe Trp
 100 105 110
 Asp Thr Leu Pro Tyr Ser Leu Ser Ser Met Gln Asn Asn Ile Ile His
 115 120 125
 Asn Ala Leu Asn Ser Asp Glu Val Leu Asn Ser Pro Leu Leu Leu Ile
 130 135 140
 Gln Val Thr Arg Leu Lys Cys Gly Gly Phe Ile Phe Gly Leu Cys Phe
 145 150 155 160
 Asn His Thr Met Ala Asp Gly Phe Gly Ile Val Gln Phe Met Lys Ala
 165 170 175
 Thr Ala Glu Ile Ala Arg Gly Ala Phe Ala Pro Ser Ile Leu Pro Val
 180 185 190
 Trp Gln Arg Ala Leu Leu Thr Ala Arg Asp Pro Pro Arg Ile Thr Phe

195	200	205	
Arg His Tyr Glu Tyr Asp Gln Val Val Asp Met Lys Ser Gly Leu Ile			
210	215	220	
Pro Val Asn Ser Lys Ile Asp Gln Leu Phe Phe Ser Gln Leu Gln			
225	230	235	240
Ile Ser Thr Leu Arg Gln Thr Leu Pro Ala His Leu His Asp Cys Pro			
245	250	255	
Ser Phe Glu Val Leu Thr Ala Tyr Val Trp Arg Leu Arg Thr Ile Ala			
260	265	270	
Leu Gln Phe Lys Pro Glu Glu Glu Val Arg Phe Leu Cys Val Met Asn			
275	280	285	
Leu Arg Ser Lys Ile Asp Ile Pro Leu Gly Tyr Tyr Gly Asn Ala Val			
290	295	300	
Val Val Pro Ala Val Ile Thr Thr Ala Ala Lys Leu Cys Gly Asn Pro			
305	310	315	320
Leu Gly Tyr Ala Val Asp Leu Ile Arg Lys Ala Lys Ala Lys Ala Thr			
325	330	335	
Met Glu Tyr Ile Lys Ser Thr Val Asp Leu Met Val Ile Lys Gly Arg			
340	345	350	
Pro Tyr Phe Thr Val Val Gly Ser Phe Met Met Ser Asp Leu Thr Arg			
355	360	365	
Ile Gly Val Glu Asn Val Asp Phe Gly Trp Gly Lys Ala Ile Phe Gly			
370	375	380	
Gly Pro Thr Thr Gly Ala Arg Ile Thr Arg Gly Leu Val Ser Phe			
385	390	395	400
Cys Val Pro Phe Met Asn Arg Asn Gly Glu Lys Gly Thr Ala Leu Ser			
405	410	415	
Leu Cys Leu Pro Pro Ala Met Glu Arg Phe Arg Ala Asn Val His			
420	425	430	
Ala Ser Leu Gln Val Lys Gln Val Val Asp Ala Val Asp Ser His Met			
435	440	445	
Gln Thr Ile Gln Ser Ala Ser Lys			
450	455		
<210> 27			
<211> 397			
<212> PRT			
<213> Fragaria x ananassa			
<223> Strawberry aminotransferase			
<400> 27			
Met Ala Lys Leu Gln Ala Gly Tyr Leu Phe Pro Glu Ile Ala Arg Arg			
1	5	10	15
Arg Asn Ala His Leu Gln Lys His Pro Asp Ala Lys Ile Ile Pro Leu			
20	25	30	

Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu Tyr Ile Thr Ser Ala
 35 40 45

Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu Glu Gly Tyr Ser Gly
 50 55 60

Tyr Gly Pro Glu Gln Gly Glu Lys Pro Leu Arg Val Ala Ile Ala Lys
 65 70 75 80

Thr Phe Tyr Gly Asp Leu Gly Ile Glu Glu Asp Asp Ile Phe Val Ser
 85 90 95

Asp Gly Ala Lys Cys Asp Ile Ser Arg Leu Gln Val Leu Phe Gly Ala
 100 105 110

Asp Lys Thr Ile Ala Val Gln Asp Pro Ser Tyr Pro Ala Tyr Val Asp
 115 120 125

Ser Ser Val Ile Met Gly Gln Thr Gly Gln Tyr Gln Lys Ser Val Gln
 130 135 140

Lys Phe Gly Asn Ile Glu Tyr Met Arg Cys Thr Pro Asp Asn Gly Phe
 145 150 155 160

Phe Pro Asp Leu Ser Ser Thr Lys Arg Thr Asp Ile Ile Phe Phe Cys
 165 170 175

Ser Pro Asn Asn Pro Thr Gly Ser Ala Ala Thr Arg Glu Gln Leu Thr
 180 185 190

Gln Leu Val Lys Phe Ala Lys Asp Asn Gly Ser Ile Ile Val Tyr Asp
 195 200 205

Ser Ala Tyr Ala Met Tyr Met Ser Asp Asp Asn Pro Arg Ser Ile Phe
 210 215 220

Glu Ile Pro Gly Ala Lys Asp Val Ala Leu Glu Thr Ser Ser Phe Ser
 225 230 235 240

Lys Tyr Ala Gly Phe Thr Gly Val Arg Leu Gly Trp Thr Val Val Pro
 245 250 255

Lys Gln Leu Gln Tyr Ser Asp Gly Phe Gln Val Ala Lys Asp Phe Asn
 260 265 270

Arg Ile Val Cys Thr Cys Phe Asn Gly Ala Ser Thr Ile Ile Gln Ala
 275 280 285

Gly Gly Leu Ala Cys Leu Gln Pro Lys Gly Val Lys Ala Met His Gly
 290 295 300

Val Ile Asn Phe Tyr Lys Glu Asn Thr Lys Ile Ile Met Glu Thr Phe
 305 310 315 320

Asn Ser Leu Gly Phe Asn Val Tyr Gly Gly Thr Asn Ala Pro Tyr Val
 325 330 335

Trp Val His Phe Pro Gly Gln Ser Ser Trp Asp Val Phe Ala Glu Ile
 340 345 350

Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe Gly Pro
 355 360 365

Gly Gly Glu Gly Phe Ile Arg Val Ser Ala Phe Gly His Arg Lys Asn
 370 375 380
 Ile Leu Glu Ala Cys Lys Arg Phe Lys Gln Leu Tyr Lys
 385 390 395
 <210> 28
 <211> 458
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry thiolase
 <400> 28
 Met Glu Lys Ala Ile Asn Arg Gln Lys Val Leu Leu Asp His Leu Arg
 1 5 10 15
 Pro Ser Ser Ser Ser Asp Asp Ser Ser Leu Ser Ala Ser Val Cys Ala
 20 25 30
 Ala Gly Asp Ser Ala Ala Tyr Ala Arg Asn His Val Phe Gly Asp Asp
 35 40 45
 Val Val Ile Val Ala Ala Phe Arg Thr Pro Leu Cys Lys Ala Lys Arg
 50 55 60
 Gly Gly Phe Lys Tyr Thr Tyr Ala Asp Asp Leu Leu Ala Pro Val Leu
 65 70 75 80
 Lys Ala Val Val Glu Lys Thr Asn Leu Asn Pro Lys Glu Val Gly Asp
 85 90 95
 Ile Val Val Gly Thr Val Leu Ala Pro Gly Ser Gln Arg Ala Ser Glu
 100 105 110
 Cys Arg Met Ala Ala Phe Tyr Ala Gly Phe Pro Glu Thr Val Pro Val
 115 120 125
 Arg Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln Ala Val Ala Asp
 130 135 140
 Val Ala Ala Ala Ile Arg Ala Gly Phe Tyr Asp Ile Gly Ile Gly Ala
 145 150 155 160
 Gly Leu Glu Ser Met Thr Ala Asn Pro Met Ala Trp Glu Gly Asp Val
 165 170 175
 Asn Pro Lys Val Lys Ile Phe Glu Gln Ala Gln Asn Cys Leu Leu Pro
 180 185 190
 Met Gly Val Thr Ser Glu Asn Val Ala His Arg Phe Gly Val Ser Arg
 195 200 205
 Gln Glu Gln Asp Gln Ala Ala Val Asp Ser His Arg Lys Ala Ala Ala
 210 215 220
 Ala Ala Ala Ala Gly Arg Phe Lys Asp Glu Ile Ile Pro Val Ala Thr
 225 230 235 240
 Lys Ile Val Asp Pro Lys Ser Gly Asp Glu Lys Pro Val Thr Ile Ser
 245 250 255
 Val Asp Asp Gly Ile Arg Asn Thr Thr Leu Ala Asp Leu Ala Lys Leu

260

265

270

Lys Pro Val Phe Lys Lys Asp Gly Thr Thr Thr Ala Gly Asn Ser Ser
 275 280 285

Gln Val Ser Asp Gly Ala Gly Ala Val Leu Leu Met Lys Arg Ser Val
 290 295 300

Ala Asp Gln Lys Gly Leu Pro Ile Leu Gly Val Phe Arg Asn Phe Val
 305 310 315 320

Ala Val Gly Val Asp Pro Ala Ile Met Gly Val Gly Pro Ala Ala Ala
 325 330 335

Ile Pro Val Ala Val Lys Ala Ala Gly Leu Glu Leu Asp Asp Ile Asp
 340 345 350

Leu Phe Glu Ile Asn Glu Ala Phe Ala Ser Gln Phe Val Tyr Cys Arg
 355 360 365

Asn Lys Leu Gly Leu Asp Pro Glu Lys Ile Asn Val Asn Gly Gly Ala
 370 375 380

Met Ala Ile Gly His Pro Leu Gly Ala Thr Gly Ala Arg Cys Val Ala
 385 390 395 400

Thr Leu Leu His Glu Met Lys Arg Arg Gly Lys Asp Cys Arg Tyr Gly
 405 410 415

Val Ile Ser Met Cys Ile Gly Thr Gly Met Gly Ala Ala Ala Val Phe
 420 425 430

Glu Arg Gly Asp Arg Thr Asp Glu Leu Cys Asn Ala Arg Lys Val Glu
 435 440 445

Ser Leu Asn Phe Leu Ser Lys Asp Val Arg
 450 455

<210> 29

<211> 605

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry pyruvate decarboxylase

<400> 29

Met Asp Thr Lys Ile Gly Ser Ile Asp Val Cys Lys Thr Glu Asn His
 1 5 10 15

Asp Val Gly Cys Leu Pro Asn Ser Ala Thr Ser Thr Val Gln Asn Ser
 20 25 30

Val Pro Ser Thr Ser Leu Ser Ser Ala Asp Ala Thr Leu Gly Arg His
 35 40 45

Leu Ala Arg Arg Leu Val Gln Ile Gly Val Thr Asp Val Phe Thr Val
 50 55 60

Pro Gly Asp Phe Asn Leu Thr Leu Leu Asp His Leu Ile Ala Glu Pro
 65 70 75 80

Gly Leu Thr Asn Ile Gly Cys Cys Asn Glu Leu Asn Ala Gly Tyr Ala
 85 90 95

Ala Asp Gly Tyr Ala Arg Ser Arg Gly Val Gly Ala Cys Val Val Thr
 100 105 110
 Phe Thr Val Gly Gly Leu Ser Val Leu Asn Ala Ile Ala Gly Ala Tyr
 115 120 125
 Ser Glu Asn Leu Pro Val Ile Cys Ile Val Gly Gly Pro Asn Ser Asn
 130 135 140
 Asp Tyr Gly Thr Asn Arg Ile Leu His His Thr Ile Gly Leu Pro Asp
 145 150 155 160
 Phe Ser Gln Glu Leu Arg Cys Phe Gln Thr Val Thr Cys Phe Gln Ala
 165 170 175
 Val Val Asn Asn Leu Glu Asp Ala His Glu Met Ile Asp Thr Ala Ile
 180 185 190
 Ser Thr Ala Leu Lys Glu Ser Lys Pro Val Tyr Ile Ser Ile Gly Cys
 195 200 205
 Asn Leu Ala Gly Ile Pro His Pro Thr Phe Ser Arg Glu Pro Val Pro
 210 215 220
 Phe Ser Leu Ser Pro Lys Leu Ser Asn Lys Trp Gly Leu Glu Ala Ala
 225 230 235 240
 Val Glu Ala Ala Ala Glu Phe Leu Asn Lys Ala Val Lys Pro Val Met
 245 250 255
 Val Gly Gly Pro Lys Leu Arg Ser Ala His Ala Gly Asp Ala Phe Val
 260 265 270
 Glu Leu Ala Asp Ala Ser Gly Phe Ala Leu Ala Val Met Pro Ser Ala
 275 280 285
 Lys Gly Gln Val Pro Glu His His Pro His Phe Ile Gly Thr Tyr Trp
 290 295 300
 Gly Ala Val Ser Thr Ala Phe Cys Ala Glu Ile Val Glu Ser Ala Asp
 305 310 315 320
 Ala Tyr Leu Phe Ala Gly Pro Ile Phe Asn Asp Tyr Ser Ser Val Gly
 325 330 335
 Tyr Ser Leu Leu Leu Lys Lys Glu Lys Ala Ile Ile Val Gln Pro Asp
 340 345 350
 Arg Val Thr Ile Gly Asn Gly Pro Thr Phe Gly Cys Val Leu Met Lys
 355 360 365
 Asp Phe Leu Leu Gly Leu Ala Lys Lys Leu Lys His Asn Asn Thr Ala
 370 375 380
 His Glu Asn Tyr Arg Arg Ile Phe Val Pro Asp Gly His Pro Leu Lys
 385 390 395 400
 Ala Ala Pro Lys Glu Pro Leu Arg Val Asn Val Leu Phe Lys His Ile
 405 410 415
 Gln Asn Met Leu Ser Ala Glu Thr Ala Val Ile Ala Glu Thr Gly Asp
 420 425 430

Ser Trp Phe Asn Cys Gln Lys Leu Lys Leu Pro Pro Gly Cys Gly Tyr
 435 440 445
 Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp Ser Val Gly Ala Thr
 450 455 460
 Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg Val Ile Ser Phe Ile
 465 470 475 480
 Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp Val Ser Thr Met Ile
 485 490 495
 Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile Asn Asn Gly Gly Tyr
 500 505 510
 Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr Asn Val Ile Lys Asn
 515 520 525
 Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His Asn Gly Glu Gly Lys
 530 535 540
 Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu Leu Ile Glu Ala Ile
 545 550 555 560
 Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe Cys Phe Ile Glu Val
 565 570 575
 Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu Leu Glu Trp Gly Ser
 580 585 590
 Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn Pro Gln
 595 600 605

<210> 30
 <211> 333
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry alcohol dehydrogenase

 <400> 30
 Met Val Met Ser Ile Glu Gln Glu His Pro Lys Lys Ala Ser Gly Trp
 1 5 10 15
 Ala Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Ser Phe Ser Arg
 20 25 30
 Arg Glu Thr Gly Glu Lys Asp Val Thr Phe Lys Val Met Tyr Cys Gly
 35 40 45
 Ile Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser
 50 55 60
 Thr Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu
 65 70 75 80
 Val Gly Ser Asn Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val
 85 90 95

Gly Cys Ile Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His
 100 105 110
 Leu Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr
 115 120 125
 Tyr Asp Gly Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala
 130 135 140
 Asp Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly
 145 150 155 160
 Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg
 165 170 175
 Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu
 180 185 190
 Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val
 195 200 205
 Lys Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Arg
 210 215 220
 Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln
 225 230 235 240
 Met Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser
 245 250 255
 Ala Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly
 260 265 270
 Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val
 275 280 285
 Phe Pro Leu Leu Met Gly Arg Lys Met Val Ala Gly Ser Gly Ile Gly
 290 295 300
 Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Lys His Asn
 305 310 315 320
 Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
 325 330
 <210> 31
 <211> 326
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry alcohol dehydrogenase
 <400> 31
 Glu Thr Gly Ala Thr Asp Val Arg Phe Lys Val Leu Tyr Cys Gly Val
 1 5 10 15
 Cys His Ser Asp Ile His Met Ala Lys Asn Asp Trp Gly Thr Ser Thr
 20 25 30
 Tyr Pro Ile Val Pro Gly His Glu Leu Val Gly Val Val Thr Glu Val
 35 40 45
 Gly Cys Lys Val Lys Lys Phe Lys Ser Trp Arg Gln Gly Arg Cys Trp

50

55

60

Leu His Gly Arg Leu Arg Pro Thr Cys Glu Asn Cys Ile His His Leu
 65 70 75 80

Glu Asn Tyr Cys Pro Asn Leu Ile Gln Thr Tyr Gly Ser Lys Tyr Tyr
 85 90 95

Asp Gly Thr Met Thr Tyr Gly Tyr Ser Asn Asn Met Val Thr Asp
 100 105 110

Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala
 115 120 125

Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Trp Arg Tyr
 130 135 140

Tyr Gly Leu Asp Lys Pro Gly Met His Leu Gly Val Glu Trp Pro Arg
 145 150 155 160

Arg Phe Arg Ser Arg Pro Pro Leu Asn Leu Pro Gly Leu Trp Gly Ser
 165 170 175

Arg Leu Gln Ser Leu Val Pro Pro Leu Ile Lys Glu Gly Ser Tyr
 180 185 190

Gly Thr Ser Pro Ala Leu Met His Ser Leu Leu Arg Thr Asp Gln Asp
 195 200 205

Gln Met Glu Ala Ala Met Ser Thr Met Asp Gly Ile Ile Asp Thr Val
 210 215 220

Pro Ala Val Arg Pro Leu Glu Pro Leu Ile Ser Leu Leu Lys Thr Asn
 225 230 235 240

Gly Lys Val Val Thr Val Gly Ile Ala Val Gln Pro Leu Asp Leu Pro
 245 250 255

Val Phe Pro Leu Ile Ile Gly Arg Lys Met Val Ala Gly Ser Ala Ile
 260 265 270

Gly Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Glu His
 275 280 285

Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu Asn Thr
 290 295 300

Ala Met Glu Arg Val Val Lys Lys Asp Val Arg Phe Arg Phe Val Ile
 305 310 315 320

Asp Val Glu Asn Thr Leu
 325

<210> 32

<211> 278

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 32

Lys Val Gln Lys Phe Lys Val Gly Asp Lys Val Gly Val Gly Cys Leu
 1 5 10 15

Val Gly Ser Cys Lys Thr Cys Asp Ser Cys Ala Asn Asp Leu Glu Asn
 20 25 30

Tyr Cys Pro Lys Gln Ile Gln Thr Tyr Gly Ala Lys Tyr Leu Asp Gly
 35 40 45

Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp Glu Ala
 50 55 60

Phe Val Ile Arg Ile Pro Asp Asn Leu Pro Leu Glu Gly Ala Ala Pro
 65 70 75 80

Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr Phe Gly
 85 90 95

Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly Gly Leu
 100 105 110

Gly His Val Ala Val Lys Phe Ala Lys Ala Leu Gly Val Asn Val Thr
 115 120 125

Val Ile Ser Thr Ser Ala Asn Lys Lys Asp Glu Ala Ile Lys His Leu
 130 135 140

Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met Gln Ala
 145 150 155 160

Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val His
 165 170 175

Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu Val
 180 185 190

Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Ser Leu
 195 200 205

Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile Lys
 210 215 220

Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr Ala
 225 230 235 240

Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu Arg
 245 250 255

Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly Asn
 260 265 270

Thr Leu Lys Pro Ala Ile
 275

<210> 33
 <211> 283
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry alcohol dehydrogenase

<400> 33
 Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Asn Phe Ser Arg Arg
 1 5 10 15

Glu Thr Gly Glu Lys Asp Val Met Phe Lys Val Leu Tyr Cys Gly Ile

20

25

30

Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr
 35 40 45

Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val
 50 55 60

Gly Ser Lys Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly
 65 70 75 80

Cys Val Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu
 85 90 95

Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr
 100 105 110

Asp Gly Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp
 115 120 125

Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala
 130 135 140

Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr
 145 150 155 160

Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly
 165 170 175

Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys
 180 185 190

Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Leu Lys
 195 200 205

His Leu Gly Ala Asp Ser Phe Phe Val Ser Arg Asp Gln Asp Gln Met
 210 215 220

Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala
 225 230 235 240

Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys
 245 250 255

Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe
 260 265 270

Pro Leu Leu Met Gly Arg Lys Met Gly Ser Trp
 275 280

<210> 34

<211> 188

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 34

Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val
 1 5 10 15

Val Gly Leu Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala
 20 25 30

Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys Asp
35 40 45

Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp
50 55 60

Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp
65 70 75 80

Thr Val Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys
85 90 95

Ala Asn Gly Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu
100 105 110

Leu Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser
115 120 125

Asn Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala
130 135 140

Lys His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
145 150 155 160

Asn Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe
165 170 175

Val Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr
180 185

<210> 35

<211> 1227

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (2)..(979)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 35

g gaa aca gga gca acg gac gta aga ttc aaa gtg ttg tac tgt gga gta 49
Glu Thr Gly Ala Thr Asp Val Arg Phe Lys Val Leu Tyr Cys Gly Val
1 5 10 15

tgc cat tcg gac ata cac atg gcc aaa aat gat tgg ggg act tct acc 97
Cys His Ser Asp Ile His Met Ala Lys Asn Asp Trp Gly Thr Ser Thr
20 25 30

tat cct att gta cct ggg cat gaa ctt gtt ggt gta gta aca gaa gta 145
Tyr Pro Ile Val Pro Gly His Glu Leu Val Gly Val Val Thr Glu Val
35 40 45

gga tgc aaa gta aag aaa ttc aaa agt tgg aga caa ggt cgg tgt tgg 193
Gly Cys Lys Val Lys Lys Phe Lys Ser Trp Arg Gln Gly Arg Cys Trp
50 55 60

ttg cat ggt cga ctc aga cca act tgc gaa aat tgt atc cat cac cta 241
Leu His Gly Arg Leu Arg Pro Thr Cys Glu Asn Cys Ile His His Leu

65	70	75	80	
gaa aat tac tgt ccg aat ctg ata caa acc tac ggt tct aaa tac tac				289
Glu Asn Tyr Cys Pro Asn Leu Ile Gln Thr Tyr Gly Ser Lys Tyr Tyr				
85	90	95		
gac gga acc atg aca tac gga ggt tac tcg aac aac atg gtg act gat				337
Asp Gly Thr Met Thr Tyr Gly Gly Tyr Ser Asn Asn Met Val Thr Asp				
100	105	110		
gag cac ttc att gtt cgg atc ccg gac aac tta cct ctt gat ggc gct				385
Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala				
115	120	125		
gct ccg ctt cta tgt gcc ggg att aca act tac agc cca tgg aga tat				433
Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Trp Arg Tyr				
130	135	140		
tat gga ctt gac aaa ccc ggt atg cat ctt ggt gtt gaa tgg cct agg				481
Tyr Gly Leu Asp Lys Pro Gly Met His Leu Gly Val Glu Trp Pro Arg				
145	150	155	160	
cggtttagg tca cgt ccg ccg tta aat ttg cca ggg ctt tgg ggc tca				529
Arg Phe Arg Ser Arg Pro Pro Leu Asn Leu Pro Gly Leu Trp Gly Ser				
165	170	175		
agg tta cag tca tta gta cct ccc cta att aaa gaa gga ggc agc tat				577
Arg Leu Gln Ser Leu Val Pro Pro Leu Ile Lys Glu Gly Ser Tyr				
180	185	190		
gga aca tct ccc gcg ctg atg cat tcc ctg ctt aga act gac caa gat				625
Gly Thr Ser Pro Ala Leu Met His Ser Leu Leu Arg Thr Asp Gln Asp				
195	200	205		
cag atg gag gct gcc atg agc aca atg gat ggt atc att gac aca gtt				673
Gln Met Glu Ala Ala Met Ser Thr Met Asp Gly Ile Ile Asp Thr Val				
210	215	220		
cct gca gtt cga cct cta gag cct ttg att tca ttg ttg aag act aat				721
Pro Ala Val Arg Pro Leu Glu Pro Leu Ile Ser Leu Leu Lys Thr Asn				
225	230	235	240	
gga aaa gtt gtt acc gtt ggt ata gca gtg cag cca ctc gat ctc cca				769
Gly Lys Val Val Thr Val Gly Ile Ala Val Gln Pro Leu Asp Leu Pro				
245	250	255		
gtt ttc cct ttg ata ata gga agg aag atg gta gct ggt agt gcc att				817
Val Phe Pro Leu Ile Ile Gly Arg Lys Met Val Ala Gly Ser Ala Ile				
260	265	270		
gga ggt atg aaa gag acg caa gag atg att gat ttt gct gct gaa cat				865
Gly Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Glu His				
275	280	285		
aac ata aca gct gac atc gag gtc atc ccg att gat tac ctg aac acc				913
Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu Asn Thr				
290	295	300		
gca atg gaa cgc gtt gtc aaa aaa gat gtc agg ttt cga ttt gtc atc				961
Ala Met Glu Arg Val Val Lys Lys Asp Val Arg Phe Arg Phe Val Ile				
305	310	315	320	

gac gtt gag aac aca ttg taagtccgcc taagttttc attcaattct 1009
 Asp Val Glu Asn Thr Leu
 325

gttaataaga ctatgcatta atatatgact gactctccat aggatggagt tatcagtctt 1069
 caaatttcta gacatatttt gtgatcaaat aatggaaatg gctttgttt cctttccac 1129
 taagattaga tttcagttgt attgtttta aagagattga tgttttatt aattgtaca 1189
 gtgttatcag tctaattcatt aaaaaaaaaa aaaaaaaaaa 1227

<210> 36
 <211> 1063
 <212> DNA
 <213> Fragaria x ananassa

<220>
 <221> CDS
 <222> (3)..(836)
 <223> partial cDNA

<220>
 <223> Strawberry alcohol dehydrogenase

<400> 36
 gc aaa gtg caa aaa ttt aaa gtt gga gac aaa gtt ggt gtt ggg tgc 47
 Lys Val Gln Lys Phe Lys Val Gly Asp Lys Val Gly Val Gly Cys
 1 5 10 15

ttg gta ggc tca tgc aaa act tgc gac agc tgc gct aac gat ttg gag 95
 Leu Val Gly Ser Cys Lys Thr Cys Asp Ser Cys Ala Asn Asp Leu Glu
 20 25 30

aac tac tgc ccc aaa cag ata cag act tac ggc gcc aag tac ctt gac 143
 Asn Tyr Cys Pro Lys Gln Ile Gln Thr Tyr Gly Ala Lys Tyr Leu Asp
 35 40 45

gga aca acc aca tac ggc ggt tac tct gac atc atg gtg gcg gat gag 191
 Gly Thr Thr Tyr Gly Tyr Ser Asp Ile Met Val Ala Asp Glu
 50 55 60

gcc ttt gta atc cgt att ccg gac aac ctg cct ctt gag ggt gct gct 239
 Ala Phe Val Ile Arg Ile Pro Asp Asn Leu Pro Leu Glu Gly Ala Ala
 65 70 75

cct ctc cta tgt gcc gga atc aca act tac agt ccc ctg agg tat ttc 287
 Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr Phe
 80 85 90 95

gga ctt gac aaa ccc ggc atg cat gtc ggg gtg gtt ggc ctt ggc ggt 335
 Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly Gly
 100 105 110

tta ggc cat gtc gcg gtg aag ttt gcc aag gct ttg ggg gtt aat gtc 383
 Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Leu Gly Val Asn Val
 115 120 125

aca gtg atc agt acc tcc gct aat aag aaa gat gaa gct att aaa cac 431
 Thr Val Ile Ser Thr Ser Ala Asn Lys Lys Asp Glu Ala Ile Lys His
 130 135 140

ctt ggt gct gat tct ttc ttg gtc agt cgt gac caa gat cag atg cag	479
Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met Gln	
145 150 155	
gct gcc atg gga aca ttg gac ggt atc atc gac aca gtt tcc gca gtc	527
Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val	
160 165 170 175	
cac ccc ctc cca cct ttg att agt tta ttg aag gct aat gga aag ctt	575
His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu	
180 185 190	
gtt atg gtt gga gca cca gag aag cca ctt gag cta cca gtt ttt tct	623
Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Ser	
195 200 205	
tta ata atg gga agg aag act tta gcc ggt agt aat atc gga ggt atc	671
Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile	
210 215 220	
aag gag aca caa gag atg ata gat ttg gca gcc aaa cac aac ata acg	719
Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr	
225 230 235	
gcc gac atc gag att atc ccc atc gac tat ttg aac act gct atg gag	767
Ala Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu	
240 245 250 255	
cgt ctt gct aaa ggg gat gtt aga tac cgt ttt gtc atc gac atc gga	815
Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly	
260 265 270	
aac aca ttg aag ccg gcc att taaatttgc a tttcgatc a aactgaatc	866
Asn Thr Leu Lys Pro Ala Ile	
275	
aagcgaggc gagaggccta cgtaacaatg caaacatgtg ctagcttgc tttggatgt 926	
tcttttagctt ttctctgatg tattccatct gttttgtca tgtcccatct tattatgaga 986	
aaaatgtggg taccgtggat attgaataaa tgaagagcta ctggaacgtat ggtttcacaa 1046	
aaaaaaaaaaaa aaaaaaaaaa 1063	
<210> 37	
<211> 1228	
<212> DNA	
<213> Fragaria x ananassa	
<220>	
<221> CDS	
<222> (1)..(849)	
<223> partial cDNA	
<220>	
<223> Strawberry alcohol dehydrogenase	
<400> 37	
gca aga gat tca tct ggt gtc ctc tct ccc ttc aat ttc tcc aga agg	48
Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Asn Phe Ser Arg Arg	
1 5 10 15	

gaa acc gga gag aaa gac gtt atg ttc aaa gtg ttg tac tgt gga att Glu Thr Gly Glu Lys Asp Val Met Phe Lys Val Leu Tyr Cys Gly Ile 20 25 30	96
tgc cat tcg gac ctt cac atg gtc aag aat gaa tgg ggc ttc tct acc Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr 35 40 45	144
tat cct ttg gtc ccg ggg cat gag att gtt ggt gaa gtt acg gaa gta Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val 50 55 60	192
ggg agc aaa gta caa aaa ttt aaa gtt gga gac aga gtc ggt gtt gga Gly Ser Lys Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly 65 70 75 80	240
tgc gtt gtg gga tct tgc cga tct tgt gaa aat tgt acc gac cac ctt Cys Val Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu 85 90 95	288
gag aac tac tgc ccc aaa cag ata ctc act tac ggt gcc aag tac tac Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr 100 105 110	336
gac gga acc acc acc tat ggc ggt tac tct gac att atg gtg gcc gac Asp Gly Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp 115 120 125	384
gaa cac ttc ata gta cgc atc cca gac aac ttg cct ctt gat ggc gct Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala 130 135 140	432
gcg ccg ctc cta tgt gcc ggg att aca acc tac agc ccc ctg aga tat Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr 145 150 155 160	480
ttc gga ctt gac aag ccc ggc atg cat gta ggt gtg gtc ggc cta ggc Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly 165 170 175	528
ggt tta ggc cac gtc gcc gtg aag ttt gcc aag gct atg gga gtg aag Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys 180 185 190	576
gtt aca gtg atc agt acg tcc cct aag aaa gag gag gaa gct ctt aaa Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Ala Leu Lys 195 200 205	624
cac cta gga gct gac tcg ttt ttc gtt agc cgt gac caa gat caa atg His Leu Gly Ala Asp Ser Phe Phe Val Ser Arg Asp Gln Asp Gln Met 210 215 220	672
cag gct gcc att ggt acc atg gat ggg atc att gac aca gtt tct gca Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala 225 230 235 240	720
caa cat cct ctc ctg cct ttg att ggt ttg ttg aag tct cat gga aag Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys 245 250 255	768
ctt gtt atg gtt ggt gca cca gag aag cct ctt gaa ctt cca gtt ttt Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe	816

260

265

270

cct tta ctc atg gga aga aag atg ggt agc tgg taaccggcat ttgggggtat 869
 Pro Leu Leu Met Gly Arg Lys Met Gly Ser Trp
 275 280

gaaggagaca caagagatga tagatttgc tgccaggcac aacataaacag cagacatcga 929
 agtcatacaa tcgactactt aaacactgct atggagcggt tagtcaaagc agatgtcaga 989
 taccgtttt tcacgacat tggaaacaca ctgaaggcta gcacttaat tctgcaatcc 1049
 agactgtatc aatgaagaaa caagaacaga aactgagatt gatttgggtgt catactccgc 1109
 ctatggttt ccttacagca tttttgttg tttgctacat gaataacgt cacatgaact 1169
 gtgatgattt gataataaaa gaatacataa aaaaaaaaaa caaaaaaaaaa aaaaaaaaaa 1228

<210> 38
 <211> 852
 <212> DNA
 <213> Fragaria x ananassa

<220>
 <221> CDS
 <222> (3)..(566)
 <223> partial cDNA

<220>
 <223> Strawberry alcohol dehydrogenase

<400> 38
 gt ccc ctg agg tat ttc gga ctt gac aaa ccc ggc atg cat gtc ggg 47
 Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly
 1 5 10 15

gtg gtt ggc ctt ggc ggt tta ggc cat gtc gcg gtg aag ttt gcc aag 95
 Val Val Gly Leu Gly Leu Gly His Val Ala Val Lys Phe Ala Lys
 20 25 30

gct ttg ggg gtt gag gtc aca gtg atc agt acc tcc gct aat aag aaa 143
 Ala Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys
 35 40 45

gat gaa gct att aaa cac ctt ggt gct gat tct ttc ttg gtc agt cgt 191
 Asp Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg
 50 55 60

gac caa gat cag atg cag gct gcc atg gga aca ttg gac ggt atc atc 239
 Asp Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile
 65 70 75

gac aca gtt tct gca gtc cac ccc ctc cca cct ttg att agt tta ttg 287
 Asp Thr Val Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu
 80 85 90 95

aag gct aat gga aag ctt gtt atg gtt gga gca cca gag aag cca ctt 335
 Lys Ala Asn Gly Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu
 100 105 110

gag cta cca gtt ttt tct tta ata atg gga agg aag act tta gcc ggt 383
 Glu Leu Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly

115	120	125	
agt aat atc gga ggt atc aag gag aca caa gag atg ata gat ttg gca			431
Ser Asn Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Ile Asp Leu Ala			
130	135	140	
gct aaa cac aac ata acg gcc gac atc gag gtc atc ccc atc gat tat			479
Ala Lys His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr			
145	150	155	
ttg aac act gca atg gag cgt ctt gct aaa ggg gat gtt aga tac cgg			527
Leu Asn Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg			
160	165	170	175
ttt gtc atc gac atc gga aac aca ttg aag ccg gcc act taaatttgca			576
Phe Val Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr			
180	185		
tttcgatcag aaactgaatc aagcgatgtc gagaggccta cgtaacaatg taaacatgtg			636
ctagctgtt ctgttagtag tcttagcat ttctctgatg tactccttct gttttgttca			696
tgttccatct tataataaga ttcttattat gaaaaaaaaa tggtaaccgtg gatattgaat			756
aaatgaagaa ctactggaac aatggttca caaattattt gtggtgctaa aaaaaaaaaa			816
aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaa aaaaaaa			852
<210> 39			
<211> 181			
<212> PRT			
<213> Fragaria x ananassa			
<223> Strawberry alcohol dehydrogenase			
<400> 39			
Phe Gly Leu Asp Val Gly Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly			
1	5	10	15
Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His His			
20	25	30	
Ile Thr Val Ile Ser Ser Asp Lys Lys Lys Lys Glu Ala Leu Glu			
35	40	45	
His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln Met			
50	55	60	
Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro Val			
65	70	75	80
Phè His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly Lys			
85	90	95	
Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser Pro			
100	105	110	
Leu Val Met Leu Gly Glu Glu Asp Asp His Arg Glu Leu Cys Gly Glu			
115	120	125	
His Glu Gly Asp Gly Gly Asp Ala Arg Val Leu Gln Arg Glu Arg Ala			
130	135	140	

Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala Phe
 145 150 155 160

Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp Cys
 165 170 175

Cys Arg Gln Gln Ser
 180

<210> 40
 <211> 176
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry alcohol dehydrogenase

<400> 40
 Val His Cys Tyr Ala Tyr Glu Gly Lys Met Gln Glu His Leu Gln Leu
 1 5 10 15

Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala
 20 25 30

Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser
 35 40 45

Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly
 50 55 60

Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln
 65 70 75 80

Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg
 85 90 95

Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys
 100 105 110

Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro
 115 120 125

Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile
 130 135 140

Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe
 145 150 155 160

Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met
 165 170 175

<210> 41
 <211> 283
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry alcohol dehydrogenase

<400> 41
 Glu Thr Thr Ile Asn Phe Gly Ser Lys Lys Ile Ala Val Val Thr Gly
 1 5 10 15

Ala Asn Lys Gly Ile Gly Leu Glu Ile Ser Lys Gln Leu Ala Ala Lys
 20 25 30

Gly Val Gly Val Val Leu Thr Ala Arg Asp Val Lys Arg Gly Thr Glu
 35 40 45

Ala Ala Glu Asn Leu Lys Ala Ser Gly Phe Ser Asp Val Val Phe His
 50 55 60

Gln Leu Asp Val Thr Glu Pro Thr Thr Ile Gly Ser Leu Ala Asn Phe
 65 70 75 80

Leu Glu Thr Gln Phe Gly Lys Leu Asp Ile Leu Val Asn Asn Ala Gly
 85 90 95

Val Val Gly Ser Val Tyr Leu Thr Ala Asp Tyr Asp Pro Val Gln Thr
 100 105 110

Tyr Glu Thr Ala Arg Asp Cys Leu Lys Thr Asn Tyr Tyr Gly Leu Lys
 115 120 125

Gln Val Thr Glu Ala Leu Val Pro Leu Leu Gln Lys Ser Glu Ala Ala
 130 135 140

Arg Ile Val Asn Val Ser Ser Gly Leu Gly Gln Leu Arg Asn Ile Gly
 145 150 155 160

Asn Glu Lys Ala Lys Lys Glu Leu Gly Asp Ala Asp Asn Leu Asn Glu
 165 170 175

Glu Lys Val Asp Lys Leu Val Glu Glu Phe Leu Glu Asp Val Lys Gln
 180 185 190

Asp Ser Ile Glu Ser Lys Gly Trp Pro Leu Ser Ile Ser Ala Tyr Ile
 195 200 205

Val Ser Lys Ala Ala Leu Asn Ala Tyr Thr Arg Leu Leu Ala Lys Lys
 210 215 220

Tyr Pro His Ile Ala Ile Asn Ala Val Gly Pro Gly Tyr Thr Lys Thr
 225 230 235 240

Asp Leu Asn Asn Asn Ser Gly Ile Leu Thr Val Glu Glu Ala Ala Val
 245 250 255

Gly Pro Val Arg Leu Ala Leu Ile Ala Glu Thr Arg Ile Ser Gly Leu
 260 265 270

Phe Phe Asn Arg Asn Glu Glu Ser Thr Phe Asp
 275 280

<210> 42
 <211> 1010
 <212> DNA
 <213> Fragaria x ananassa

<220>
 <221> CDS
 <222> (2)..(850)
 <223> partial cDNA

<220>
 <223> Strawberry alcohol dehydrogenase

<400> 42

g gaa act acc atc aat ttt ggg tct aag aag att gca gtt gtt act gga	49
Glu Thr Thr Ile Asn Phe Gly Ser Lys Lys Ile Ala Val Val Thr Gly	
1 5 10 15	
gcc aac aaa ggg att gga ctt gag att agc aag caa tta gct gct aaa	97
Ala Asn Lys Gly Ile Gly Leu Glu Ile Ser Lys Gln Leu Ala Ala Lys	
20 25 30	
gga gtt ggg gtg gta tta aca gca aga gat gtg aag aga gga aca gaa	145
Gly Val Gly Val Val Leu Thr Ala Arg Asp Val Lys Arg Gly Thr Glu	
35 40 45	
gct gct gaa aat ctt aag gct tct ggg ttc tct gat gtg gta ttt cat	193
Ala Ala Glu Asn Leu Lys Ala Ser Gly Phe Ser Asp Val Val Phe His	
50 55 60	
cag cta gat gta aca gag ccg act act att ggt tct ttg gca aac ttt	241
Gln Leu Asp Val Thr Glu Pro Thr Thr Ile Gly Ser Leu Ala Asn Phe	
65 70 75 80	
ctt gaa acg caa ttt gga aag ctt gac ata ttg gtt aac aat gca gga	289
Leu Glu Thr Gln Phe Gly Lys Leu Asp Ile Leu Val Asn Asn Ala Gly	
85 90 95	
gtc gtt gga tct gta tac ctc aca gcc gac tat gat cca gtg caa aca	337
Val Val Gly Ser Val Tyr Leu Thr Ala Asp Tyr Asp Pro Val Gln Thr	
100 105 110	
tac gag aca gcg agg gat tgt ttg aaa aca aac tat tat ggg ctc aag	385
Tyr Glu Thr Ala Arg Asp Cys Leu Lys Thr Asn Tyr Tyr Gly Leu Lys	
115 120 125	
caa gtc aca gaa gca ctt gtt ccg ctg ctt caa aaa tct gaa gct gca	433
Gln Val Thr Glu Ala Leu Val Pro Leu Leu Gln Lys Ser Glu Ala Ala	
130 135 140	
agg ata gtc aat gtc tct tcc gga tta gga cag cta aga aat att gga	481
Arg Ile Val Asn Val Ser Ser Gly Leu Gly Gln Leu Arg Asn Ile Gly	
145 150 155 160	
aat gag aag gcc aag aag gag cta gga gat gca gat aac ctc aac gag	529
Asn Glu Lys Ala Lys Lys Glu Leu Gly Asp Ala Asp Asn Leu Asn Glu	
165 170 175	
gag aaa gtg gac aag cta gtt gag gaa ttt ctg gag gat gtg aaa cag	577
Glu Lys Val Asp Lys Leu Val Glu Glu Phe Leu Glu Asp Val Lys Gln	
180 185 190	
gat tcg ata gaa tcc aaa ggc tgg cct cta agt ata tct gcc tac att	625
Asp Ser Ile Glu Ser Lys Gly Trp Pro Leu Ser Ile Ser Ala Tyr Ile	
195 200 205	
gtc tca aaa gca gct ctg aat gct tat aca aga ctc ttg gca aag aag	673
Val Ser Lys Ala Ala Leu Asn Ala Tyr Thr Arg Leu Leu Ala Lys Lys	
210 215 220	
tat ccc cat att gcc ata aac gca gtt ggt cca ggt tat acc aaa aca	721
Tyr Pro His Ile Ala Ile Asn Ala Val Gly Pro Gly Tyr Thr Lys Thr	
225 230 235 240	
gac ctc aat aat aat tcc ggg att ctc aca gtt gaa gaa gct gca gta	769
Asp Leu Asn Asn Ser Gly Ile Leu Thr Val Glu Glu Ala Ala Val	

245

250

255

ggt cct gtg agg ctg gct ttg ata gcc gaa act aga att tcc ggc ctc 817
 Gly Pro Val Arg Leu Ala Leu Ile Ala Glu Thr Arg Ile Ser Gly Leu
 260 265 270

ttc ttc aac aga aat gaa gag tcg acc ttt gat taggtcaacg tgatccctga 870
 Phe Phe Asn Arg Asn Glu Glu Ser Thr Phe Asp
 275 280

tgaactggac tatttagat ttccagaatg tgcttgattt tgttgaagta tttatggat 930
 ttgtatgtat actttgatgt atcattgtat taatagagca catgttgtga tcaaaaaaaa 990
 aaaaaaaaaa aaaaaaaaaa 1010

<210> 43
 <211> 243
 <212> PRT
 <213> Mangifera indica
 <223> Mango esterase

<400> 43
 Met Arg Pro Gln Ile Val Leu Phe Gly Asp Ser Ile Thr Glu Gln Ser
 1 5 10 15

Phe Gly Ser Gly Gly Trp Gly Ser Ser Leu Ala Asp Thr Tyr Ser Arg
 20 25 30

Lys Ala Asp Val Leu Val Arg Gly Tyr Gly Gly Tyr Asn Thr Arg Trp
 35 40 45

Ala Leu Phe Leu Leu Cys His Ile Phe Pro Leu His Asn Lys Ile Pro
 50 55 60

Pro Ala Val Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Leu
 65 70 75 80

Gly Arg Thr Ser Glu Arg Gln His Val Pro Val Glu Glu Tyr Lys Asn
 85 90 95

Asn Leu Arg Lys Met Val Gln His Leu Lys Glu Val Ser Pro Thr Met
 100 105 110

Leu Val Val Leu Ile Thr Pro Pro Ile Asp Glu Glu Gly Arg Lys
 115 120 125

Ala Tyr Ala Arg Ser Val Tyr Gly Glu Lys Ala Met Lys Glu Pro Glu
 130 135 140

Arg Thr Asn Glu Met Ala Gly Val Tyr Ala Arg His Cys Val Glu Leu
 145 150 155 160

Ala Lys Asp Leu Pro Ala Ile Asp Leu Trp Ser Lys Met Gln Glu Thr
 165 170 175

Glu Gly Trp Gln Lys Lys Phe Leu Ser Asp Gly Leu His Leu Lys Ser
 180 185 190

Glu Gly Asn Ala Val Val His Gln Glu Val Val Arg Val Leu Lys Glu
 195 200 205

Ala Trp Phe Ser Pro Glu Gln Met Pro Tyr Asp Phe Pro His Gln Ser
210 215 220

Val Ile Asp Gly Lys His Pro Glu Lys Ala Phe Gln Leu Gln Cys Pro
225 230 235 240

Ala Glu Phe

<210> 44

<211> 877

<212> DNA

<213> Mangifera indica

<220>

<221> CDS

<222> (1)..(729)

<223> cDNA

<220>

<223> Mango esterase

<400> 44

atg agg cca caa ata gtg tta ttc gga gat tca ata acg gag caa tct 48
Met Arg Pro Gln Ile Val Leu Phe Gly Asp Ser Ile Thr Glu Gln Ser
1 5 10 15

ttc gga tca ggt ggt tgg ggt tct tct ctt gct gac act tac tct cgc 96
Phe Gly Ser Gly Trp Gly Ser Ser Leu Ala Asp Thr Tyr Ser Arg
20 25 30

aag gct gat gta tta gtt cgt ggc tat ggt ggc tac aat act aga tgg 144
Lys Ala Asp Val Leu Val Arg Gly Tyr Gly Gly Tyr Asn Thr Arg Trp
35 40 45

gca ttg ttc ttg tta tgt cac att ttc cct ctg cac aat aaa ata cct 192
Ala Leu Phe Leu Leu Cys His Ile Phe Pro Leu His Asn Lys Ile Pro
50 55 60

cca gcc gtc acc aca att ttc ttt ggg gct aat gat gca gcc ctt ctt 240
Pro Ala Val Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Leu
65 70 75 80

ggg aga acg agt gaa agg cag cat gtt ccc gtg gaa gaa tac aag aac 288
Gly Arg Thr Ser Glu Arg Gln His Val Pro Val Glu Glu Tyr Lys Asn
85 90 95

aat ctc aga aaa atg gtt cag cat ttg aag gaa gtc tcc ccc acg atg 336
Asn Leu Arg Lys Met Val Gln His Leu Lys Glu Val Ser Pro Thr Met
100 105 110

cta gtt gtg ctt att act cca cca cca att gat gag gaa ggg cgt aaa 384
Leu Val Val Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu Gly Arg Lys
115 120 125

gca tat gca cga tcc gtt tat ggt gag aaa gct atg aaa gag cct gag 432
Ala Tyr Ala Arg Ser Val Tyr Gly Glu Lys Ala Met Lys Glu Pro Glu
130 135 140

agg aca aat gaa atg gct gga gtt tat gct aga cat tgt gtt gaa ctg 480
Arg Thr Asn Glu Met Ala Gly Val Tyr Ala Arg His Cys Val Glu Leu
145 150 155 160

gca aaa gat ctt cct gcc att gat ctg tgg tcc aag atg cag gaa aca	528
Ala Lys Asp Leu Pro Ala Ile Asp Leu Trp Ser Lys Met Gln Glu Thr	
165 170 175	
gaa ggt tgg cag aaa aaa ttc ctc agt gat ggg ttg cac ctt aag tca	576
Glu Gly Trp Gln Lys Lys Phe Leu Ser Asp Gly Leu His Leu Lys Ser	
180 185 190	
gaa ggc aat gca gtg gtt cac caa gaa gtt gtg aga gtt cta aaa gaa	624
Glu Gly Asn Ala Val Val His Gln Glu Val Val Arg Val Leu Lys Glu	
195 200 205	
gca tgg ttt tct cct gaa caa atg cca tat gat ttt cct cac caa tca	672
Ala Trp Phe Ser Pro Glu Gln Met Pro Tyr Asp Phe Pro His Gln Ser	
210 215 220	
gta att gat gga aaa cac cct gag aaa gct ttc caa ctg caa tgc cct	720
Val Ile Asp Gly Lys His Pro Glu Lys Ala Phe Gln Leu Gln Cys Pro	
225 230 235 240	
gct gaa ttc tagtcaagac aggcttggaa atttgttctc tctttcaatt	769
Ala Glu Phe	
tttctatttg atgaaaagat ttggactgct ttttcctagt catgccaaat gaaacagtgt	829
tagccttttg cctattttat cagatgctga tatgcgctct gtgtcgac	877
<210> 45	
<211> 12	
<212> PRT	
<213> Unknown Organism	
<220>	
<223> Description of Unknown Organism: various fruit	
<220>	
<223> alcohol acyl transferase motif	
<400> 45	
Trp Thr Asn Phe Phe Asn Pro Leu Asp Phe Gly Trp	
1 5 10	
<210> 46	
<211> 10	
<212> PRT	
<213> Unknown Organism	
<220>	
<223> Description of Unknown Organism: various fruit	
<220>	
<223> alcohol acyl transferase motif	
<220>	
<223> Xaa = any amino acid residue	
<400> 46	
Leu Xaa Xaa Xaa Tyr Pro Xaa Xaa Gly Arg	
1 5 10	
<210> 47	
<211> 16	

```

<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: various fruit

<220>
<223> alcohol acyl transferase motif

<220>
<223> Xaa = any amino acid residue

<400> 47
Pro Ser Arg Val Xaa Xaa Val Thr Xaa Phe Leu Xaa Lys Xaa Leu Ile
1 5 10 15

<210> 48
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221>
<222>
<223> PCR Primer

<220>
<223> PCR Primer

<400> 48
ggwtggggik ctaytcttgc 20

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221>
<222>
<223> PCR Primer

<220>
<223> AAP165

<400> 49
cggatccgga gaaaatttgag gtcag 25

<210> 50
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221>
<222>
<223> PCR Primer

<220>
<223> AAP166

<400> 50

```

cgtcgaccat tgcacgagcc acataatc

28